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OM protein - protein search, using sw model

Run on: August 6, 2003, 09:30:44 ; Search time 84 Seconds
(without alignments)
345.797 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPYKEFGATVLLFLP.....RRRSQSPRRRSQSPRESQC 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*

1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	971	100.0	183	18 AAW09044	Hepatitis B virus
2	956	98.5	183	20 AAY29674	Human hepatitis B
3	956	98.5	183	23 ABG94182	Hepatitis B capsid
4	956	98.5	183	23 ABG80494	Hepatitis B virus
5	956	98.5	183	23 AAU93961	Hepatitis B virus
6	956	98.5	183	23 AAU87796	Human hepatitis B
7	956	98.5	183	23 AAU80906	Hepatitis B virus
8	956	98.5	194	19 AAW50242	Hepatitis B virus
9	956	98.5	212	19 AAW50250	Hepatitis B virus

10	956	98.5	212	23 AAE19793	Hepatitis B virus
11	956	98.5	212	23 AAE19898	Hepatitis B virus
12	956	98.5	212	23 AAE17018	Hepatitis B virus
13	956	98.5	346	13 AAR27473	SL2/core protein.
14	954	98.2	183	23 ABG94185	Hepatitis B capsid
15	954	98.2	183	23 ABG80497	Hepatitis B virus
16	954	98.2	183	23 ABG80909	Hepatitis B capsid
17	953	98.1	183	23 ABG94187	Hepatitis B capsid
18	953	98.1	183	23 ABG94188	Hepatitis B virus
19	953	98.1	183	23 ABG80499	Hepatitis B virus
20	953	98.1	183	23 ABG80500	Hepatitis B virus
21	953	98.1	183	23 AAU80911	Hepatitis B virus
22	953	98.1	183	23 AAU80912	HBV genotype D pre
23	953	98.1	212	22 AAG66924	Hepatitis B capsid
24	953	98.1	212	22 AAG64190	Hepatitis B capsid
25	953	98.1	212	23 ABG94191	Hepatitis B capsid
26	953	98.1	212	23 ABG94192	Hepatitis B virus
27	953	98.1	212	23 ABG80502	Hepatitis B virus
28	953	98.1	212	23 ABG80503	Hepatitis B virus
29	953	98.1	212	23 ABG80504	Hepatitis B virus
30	953	98.1	212	23 AAU80914	Hepatitis B virus
31	953	98.1	212	23 AAU80915	Hepatitis B virus
32	953	98.1	212	23 AAU80916	Hepatitis B virus
33	951	97.9	212	23 ABG94195	Hepatitis B capsid
34	951	97.9	212	23 ABG94196	Hepatitis B capsid
35	951	97.9	212	23 ABG94197	Hepatitis B capsid
36	951	97.9	212	23 ABG80507	Hepatitis B virus
37	951	97.9	212	23 ABG80508	Hepatitis B virus
38	951	97.9	212	23 ABG80509	Hepatitis B virus
39	951	97.9	212	23 AAU80919	Hepatitis B virus
40	951	97.9	212	23 AAU80920	Hepatitis B virus
41	951	97.9	212	23 AAU80921	Hepatitis B virus
42	950	97.8	212	23 ABG94198	Hepatitis B capsid
43	950	97.8	212	23 ABG94199	Hepatitis B capsid
44	950	97.8	212	23 ABG94200	Hepatitis B capsid
45	950	97.8	212	23 ABG80510	Hepatitis B virus

ALIGNMENTS

RESULT 1

AAW09044

ID AAW09044 standard; Protein; 183 AA.

XX AC AAW09044;

XX XX

DT 11-APR-1997 (first entry)

XX Hepatitis B virus core protein.

DE

XX Hepadnavirus; HBV; woodchuck hepatitis virus; hepatitis delta virus;

KW ground squirrel hepatitis B virus; duck hepatitis B virus;

KW core protein; replication; antiviral; gene therapy.

XX Hepatitis B virus.

OS

XX Key Location/Qualifiers

FT Misc-difference 71..180

FT /note= "C-terminus of core protein is at any amino

FT acid position between 71-180 in mutant

FT polypeptides of the invention (Claim 23);"

FT

FT Misc-difference 81..180

FT /note= "C-terminus of core protein is at any amino

FT acid position between 81 and 180 in mutant

FT polypeptides of the invention (Claim 5);"

FT

FT Misc-difference 171..180

FT /note= "C-terminus of core protein is at any amino

FT acid position between 171 and 180 in mutant

FT polypeptides of the invention (Claim 6);"

FT

FT Misc-difference 174..180

FT /note= "C-terminus of core protein is at any amino

FT acid position between 174 and 180 in mutant

FT

FT	Misc-difference 178	polypeptides of the invention (Claim 26)"
FT	FT	
FT	FT	"C-terminus of core protein is at amino acid
FT	FT	position 178 in mutant polypeptides of the
FT	FT	invention (Claim 7)." /note=
FT	Misc-difference 178	
FT	FT	
FT	FT	"C-terminus of core protein is at amino acid
FT	FT	position 178 in mutant polypeptides of the
FT	FT	invention (Claim 7)." /note=
FT	Misc-difference 172..183	
FT	FT	"amino acid residues 172-183, pref. 174-180,
FT	FT	are deleted from the core protein in mutant
FT	FT	polypeptides of the invention"
XX	XX	
PN	WO9700698-A1.	
XX	XX	
PD	09-JAN-1997.	
XX	XX	
PF	20-JUN-1996; 96WO-US10602.	
XX	XX	
PR	20-JUN-1995; 95US-0017814.	
XX	XX	
PA	(GEO) GEN HOSPITAL CORP.	
XX	XX	
PI	Melegari M, Scaglioni PP, Wands JR;	
XX	XX	
DR	WPI: 1997-087176/08.	
DR	N-PSDB; AA749594.	
XX	XX	
PT	PT	New method for inhibiting the replication of hepadnaviruses -
PT	PT	comprises introducing a mutant polypeptide with a mutated core
PT	PT	protein or corresponding nucleic acid, for treating, e.g. hepatitis
PT	PT	B

XX	AA29674;	
XX	AC	
XX	XX	
XX	DT	08-NOV-1999 (first entry)
XX	XX	
DE	Human hepatitis B core protein.	
XX	XX	
KW	Human hepatitis B core protein; Hbc; modified; immunodominant; nucleocapsid protein; vaccine; T cell epitope.	
XX	XX	
OS	Hepatitis B virus.	
XX	XX	
PN	WO9940934-A1.	
XX	XX	
PD	19-AUG-1999.	
XX	XX	
PF	11-FEB-1999; 99WO-US03055.	
XX	XX	
PR	12-FEB-1998; 98US-0074537.	
XX	XX	
PA	(IMMU-) IMMUNE COMPLEX CORP.	
XX	XX	
PI	Birkett AJ;	
XX	XX	
DR	WPI; 1999-527340/44.	
DR	N-PSDB; AAZ08816.	
XX	XX	
PT	Conjugate of hepatitis B core protein, modified to increase reactivity with haptens, used to raise antibodies against the haptens, e.g. in vaccines	
PT	XX	
XX	XX	
PS	Claim 17; Page 77-78; 128pp; English.	
XX	XX	
CC	The present invention describes a conjugate (A) comprising a strategically modified hepatitis B core (Hbc) protein (I) attached to a hapten, where (I) includes amino acids (aa) 10-140 of the wild type Hbc 183 aa sequence (given in AA29674) and additionally has an insert (II) in the region corresponding to aa's 50-100, where the insert is of 1 to about 40 aa's and contains a chemically reactive aa residue linked to the haptens. A vaccine containing (A), optionally in the form of particles, is used to induce a protective antibody response against the pathogen from which the haptens is derived, in humans or other animals. These pathogens may be bacteria, viruses, rickettsia or protozoa. Insertion of (II) overcomes the low reactivity of aa side chains in native Hbc protein, increasing the reactivity with haptens and resulting in conjugates of improved immunogenicity. Modified Hbc can be derivatised in the form of particles by well-defined chemical methods, and is unlikely to cause immunological side-effects. The present sequence represents the wild type Hbc protein.	

RESULT 3
 ABG94182
 ID ABG94182 standard; Protein; 183 AA.
 XX
 AC ABG94182;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE Hepatitis B capsid (core) protein antigen (HBcAg) variant #11.
 XX
 KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
 KW cytosolic; antiviral; antidiabetic; hypoglycaemic; antigen array;
 KW vaccine; infectious disease.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200256905-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-IB00166.
 XX
 PR 19-JAN-2001; 2001US-262379P.
 PR 04-MAY-2001; 2001US-288549P.
 PR 05-OCT-2001; 2001US-326998P.
 PR 07-NOV-2001; 2001US-331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
 PI Piossek C;
 XX
 DR WPI; 2002-627351/67.
 XX
 PT Molecular antigen array used in the production of vaccines for
 PT infectious diseases -
 XX
 PS Claim 112; Page 337-338; 441pp; English.
 XX
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The
 CC invention also discloses a composition comprising a non-natural
 CC molecular scaffold comprising a core particle selected from a core
 CC particle of a non-natural origin and a core particle of natural origin
 CC and an organiser comprising at least one first attachment site, where
 CC the organiser is connected to the core particle by at least one covalent
 CC bond. Also disclosed is an antigen or antigenic determinant with at
 CC least one second attachment site, where the antigen or antigenic
 CC determinant is amyloid beta peptide (Abeta1-42) or its fragment and
 CC where the second attachment site is selected from an attachment site not
 CC naturally occurring with the antigen or antigenic determinant and an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC The invention also comprises a coat protein capable of forming a capsid
 CC which comprises mutant Qbeta coat proteins having an amino acid sequence
 CC selected from five amino acid sequences fully defined in the
 CC specification. The compounds of the invention may have antimicrobial,
 CC antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic,
 CC or hypoglycaemic activities and may be used in immunisation and as a
 CC vaccine. The present sequence represents a protein sequence used to
 CC create the compositions of the invention.
 XX
 SQ Sequence 183 AA;
 XX
 Query Match 98.5%; Score 956; DB 23; Length 183;
 Best Local Similarity 98.9%; Pred. No. 8.5e-95;
 Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVELLSFLPSDFPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MDIDPYKEFGATVELLSFLPSDFPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLSVSYVNTNMGKPKRQLLWPHISCLTFGTETVIELV 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 CWGELMTLATWGVNLEDPASRDLSVSYVNTNMGKPKRQLLWPHISCLTFGTETVIELV 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGSPRRRTSPRRRSQSPRRRSQSPRE 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGSPRRRTSPRRRSQSPRRRSQSPRE 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 SQC 183
 |||||
 Db 181 SQC 183
 |||||
 RESULT 4
 ABG80494
 ID ABG80494 standard; Protein; 183 AA.
 XX
 AC ABG80494;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Hepatitis B virus core capsid protein, HBcAg, variant #11.
 XX
 KW Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-IB00168.
 XX
 PR 19-JAN-2001; 2001US-262379P.
 PR 04-MAY-2001; 2001US-288549P.
 PR 05-OCT-2001; 2001US-326998P.
 PR 07-NOV-2001; 2001US-331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEO) LUEOEND R.
 PA (STAU) STAUFENBIEL M.
 PA (FREY) FREY P.
 XX
 PI Maurer P, Lechner F, Ortman R, Lueoend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 XX
 DR WPI; 2002-636514/68.
 XX
 PT Molecular antigen array used in the production of vaccines for
 PT infectious diseases -
 XX
 PS Claim 14; Page 314-315; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from:
 CC (1) a core particle of a non-natural origin; and (2) a core particle of
 CC natural origin; and (ii) an organiser comprising at least one first

CC attachment site, where the organism is connected to the core particle by
 CC at least one covalent bond; (b) an antigen or antigenic determinant with
 CC at least one second attachment site, where the antigen or antigenic
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and
 CC where the second attachment site is selected from: (i) an attachment site
 CC not naturally occurring with the antigen or antigenic determinant; and
 CC (ii) an attachment site naturally occurring with the antigen or
 CC antigenic determinant, where the second attachment site is capable of
 CC association through at least one non-peptide bond to the first attachment
 CC site; and where the antigen or antigenic determinant and the scaffold
 CC interact through the association to form an ordered and repetitive
 CC antigen array. Also included is a process for producing a non-naturally
 CC occurring ordered and repetitive antigen array. The composition is used
 CC in immunisation and as a vaccine for diseases such as influenza,
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, grave's
 CC disease, systemic lupus erythematosus, inflammatory immune diseases,
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's
 CC disease, osteoporosis and infectious diseases. The present sequence is
 CC an antigen for use in the array of the invention. The antigen is
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a
 CC cysteine- containing N- or C-terminal linker peptide which serves as the
 CC attachment point to a virus like particle or bacterial protein (the
 CC scaffold protein).

XX Sequence 183 AA;

Query Match 98.5%; Score 956; DB 23; Length 183;
 Best Local Similarity 98.9%; Pred. No. 8.5e-95;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWVGVNLEDPASRDVSVYVNTNMGKLFROLLWFHISCLTFGTETVIEYLV 120
 DB 61 CWGELMTLATWVGVNLEDPASRDVSVYVNTNMGKLFROLLWFHISCLTFGTETVIEYLV 120

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRE 180
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRE 180

QY 181 SQC 183
 DB 181 SQC 183

RESULT 5

AAU93961
 ID AAU93961 standard; Peptide; 183 AA.
 XX
 AC AAU93961;
 DT 02-JUL-2002 (first entry)
 XX
 DE Hepatitis B virus Hbc epitope #1.
 XX
 KW Immunogenic; hepadnavirus nucleocapsid protein; hepatitis B core; Hbc;
 KW vaccine; B cell epitope; T cell epitope; immunostimulant.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200214478-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 16-AUG-2001; 2001WO-US41759.
 XX
 PF 16-AUG-2000; 2000US-225843P.

PR 22-AUG-2000; 2000US-226867P.
 PR 15-AUG-2001; 2001US-0930915.
 XX
 PA (APOV-) APOVIA INC.
 XX
 PI Birkett AJ;
 XX
 DR WPI; 2002-257601/30.
 XX
 XX Novel recombinant hepadnavirus nucleocapsid protein, termed as chimeric
 PT hepatitis B core protein, displays immunogenic epitopes at N-terminus,
 PT Hbc immunogenic loop with linker for conjugated epitope and C-terminus
 PT
 PS Disclosure; Figure 7; 289pp; English.
 XX
 CC The invention relates to a recombinant hepadnavirus nucleocapsid protein,
 CC i.e. a chimeric hepatitis B core (Hbc) protein (I), displaying one or
 CC more immunogenic epitopes at the N-terminus, Hbc immunogenic loop (L) or
 CC C-terminus, or having a heterologous linker for a conjugated epitope in
 CC (L), and containing a Cys residue at, or near, the C-terminus that
 CC confers enhanced stability to the particles. A vaccine comprising (I) is
 CC useful for inducing an immune response in an inoculated host animal, by
 CC inoculating a host animal with the vaccine, and maintaining that
 CC inoculated animal for a time period sufficient for that animal to
 CC develop an immune response. The immunogenic particles formed using (I)
 CC are substantially free of binding to nucleic acids, and are most stable
 CC than the particle formed from otherwise identical Hbc chimera that lacks
 CC the C-terminal residue or in which a C-terminal Cys is replaced by
 CC another residue. The chimera particles are most stable on storage in
 CC aqueous compositions that are particles of similar sequence that lack any
 CC C-terminal Cys residues. The chimera molecule exhibits the self-assembly
 CC not exhibiting the nucleic acid binding of those native particles, and
 CC excellent B cell and T cell immunogenicities. The chimera particles are
 CC typically prepared in higher yield than similar particles that are free
 CC of a C-terminal Cys. The particles are often far more immunogenic than
 CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of
 CC particles assembled from the chimera molecules are enhanced as compared to
 CC similar particles assembled from chimera molecules lacking at least one
 CC C-terminal Cys. AAU93802-AAU93997 represent immunogenic Hbc particles
 CC amino acid sequences and related sequences of the invention.

XX Sequence 183 AA;

Query Match 98.5%; Score 956; DB 23; Length 183;
 Best Local Similarity 98.9%; Pred. No. 8.5e-95;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWVGVNLEDPASRDVSVYVNTNMGKLFROLLWFHISCLTFGTETVIEYLV 120
 DB 61 CWGELMTLATWVGVNLEDPASRDVSVYVNTNMGKLFROLLWFHISCLTFGTETVIEYLV 120

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRE 180
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRE 180

QY 181 SQC 183
 DB 181 SQC 183

RESULT 6
 AAU87796
 ID AAU87796 standard; Protein; 183 AA.
 XX
 AC AAU87796;
 XX
 DT 21-MAY-2002 (first entry)
 XX

DE Human hepatitis B virus nucleocapsid protein #1.
XX
KW Hepatitis B virus; nucleocapsid protein; HBC; hepatitis B virus core;
KW B cell epitope; T cell epitope; malaria; HIV-1; Plasmodium; protozoacide;
KW circumsporozoite; human immunodeficiency virus type I; human; squirrel;
KW woodchuck.
XX
OS Homo sapiens.
XX
PN WO200213765-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-US25625.
XX
PR 16-AUG-2000; 2000US-225813P.
PR 15-AUG-2001; 2001US-0931325.
XX
XX (APOV-) APOVIA INC.
XX PA
XX Birkett AJ;
XX
XX WPI; 2002-241832/29.
DR N-PSDB; ABK44278.
XX
XX Recombinant hepatitis B virus core protein chimera molecule, useful to
PT induce antibodies to malarial parasites, comprises malaria-specific
PT T-cell epitope and is engineered for enhanced stability -
XX
XX Disclosure: Fig 6; 197pp; English.
XX
XX The invention relates to a recombinant hepatitis B virus core (HBC)
CC protein chimera molecule that contains 4 peptide-linked amino acid residue
CC sequence domains. The molecule of the invention contains a region
CC constituting a B cell epitope of the circumsporozoite protein of a
CC species of the parasite, Plasmodium. The chimera sequence is useful as an
CC immunogen for inducing antibodies to the malaria-causing parasite,
CC Plasmodium, particularly P. falciparum and P. vivax. Sequences
CC AAU87695-AAU87804 represent peptide epitopes of the invention.
XX
XX Sequence 183 AA;
XX
Query Match 98.5%; Score 956; DB 23; Length 183;
Best Local Similarity 98.9%; Pred. No. 8.5e-95;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVNDLDTASALYREALSPHCHSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVNDLDTASALYREALSPHCHSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLVSVVNTNMGKLFQALLWFHISCLTFCGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLVSVVNTNMGKLFQALLWFHISCLTFCGTETVIEYLV 120
QY 121 SFGWIRTPPAYRPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSR 180
Db 121 SFGWIRTPPAYRPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSR 180
QY 181 SQC 183
Db 181 SQC 183
RESULT 7
AAU80906
ID AAU80906 standard; Protein; 183 AA.
XX AC
XX AAU80906;
XX
XX 09-APR-2002 (first entry)
DT
XX Hepatitis B virus core antigen variant (HBCag) #11.
XX

KW Vaccine; molecular scaffold; pilus; pilin; HBCag; antigen;
KW hepatitis B virus capsid protein; JUN; FOS; HIV gpl40;
KW measles virus N protein; bee venom phospholipase; Th type 2 T-helper;
KW Th2; Sinbis virus E2 protein; amyloid beta; influenza M2 antigen;
KW human immunodeficiency virus infection; viral hepatitis; measles;
KW chicken pox; pneumonia; tuberculosis; syphilis; malaria; allergy;
KW cancer; chronic disease; arthritis; colitis; diabetes;
KW multiple sclerosis.
XX
XX Hepatitis B virus.
OS
XX WO200185208-A2.
PN
XX 15-NOV-2001.
PD
XX 02-MAY-2001; 2001WO-IB00741.
PF
XX 05-MAY-2000; 2000US-202341P.
PR
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PA (SEBB/) SEBBEL P.
XX PA (DUNAN/) DUNANT N.
XX PA (BACH/) BACHMANN M.
XX PA (TISS/) TISSOT A.
XX PA (LECH/) LECHENER F.
XX
XX Sebbel P, Dunant N, Bachmann M, Tissot A, Lechener F;
PI WPI; 2002-055561/07.
XX
XX New composition, useful for vaccine production, comprises antigen or
PT antigenic determinant and non-natural molecular scaffold comprising
PT organizer and core particle such as bacterial pilus or pilin protein
PT -s
XX
XX Claim 34; Page 216-217; 287pp; English.
XX
XX The invention relates to a composition comprising: (a) a non-natural
CC molecular scaffold (molecular scaffold) which comprises a core
CC particle such as a bacterial pilus or pilin protein, a recombinant form
CC of the protein, a virus-like particle or a hepatitis B virus capsid
CC protein (HBCag), and an organizer; and (b) an antigen or antigenic
CC determinant, where the molecular scaffold and antigenic determinant
CC interact to form an ordered and repetitive antigen array. Suitable
CC antigenic determinants include JUN, FOS, HIV gpl40, measles virus N
CC protein, bee venom phospholipase, Sinbis virus E2 protein, amyloid beta
CC derived peptides and influenza M2 antigen. The composition (or vaccine)
CC is useful for immunisation, by administration to a subject, where the
CC administration produces an immune response, such as humoral, cellular or
CC protective immune response, preferably a Th type 2 T-helper (Th2)
CC response that is specific for the antigenic determinant. The
CC administration induces antibodies specific for the antigenic determinant.
CC of a subtype corresponding to the Th2 subtype in the subject. The subject
CC does not generate a Th2 subtype that is specific for pilus or pilin
CC polypeptide or antigenic determinant. The composition is useful for the
CC production of vaccines for prevention of infectious diseases such as
CC human immunodeficiency virus, viral hepatitis, measles, chicken pox,
CC pneumonia, tuberculosis, syphilis, malaria, and for treating allergy,
CC cancer, and chronic diseases induced or accelerated by a Th1 type
CC immune response, such as arthritis, colitis, diabetes and multiple
CC sclerosis. The composition is useful to generate defined self-specific
CC antibodies and specific immune responses of the Th2 type and allows the
CC creation of highly efficient vaccines against infectious diseases, and
CC for treating allergy, cancer, and chronic diseases induced or accelerated
CC by a Th1 type immune response. The present sequence is a peptide or
CC protein incorporated into the compositions of the invention.
XX
XX Sequence 183 AA;
XX

Query Match 98.5%; Score 956; DB 23; Length 183;
Best Local Similarity 98.9%; Pred. No. 8.5e-95;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDIDPYKRGATVVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKRGATVVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
OY 61 CWGELMTLATWVGVLNLEDPASRDLYVSYVNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120
Db 61 CWGELMTLATWVGVLNLEDPASRDLYVSYVNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120
OY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSOSPRRRRSQSRE 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSOSPRRRRSQSRE 180
OY 181 SOC 183
Db 181 SOC 183

RESULT 8

AAW50242
ID AAW50242 standard; Protein; 194 AA.

XX
AC AAW50242;

XX
DT 28-SEP-1998 (first entry)

XX DE Hepatitis B virus precore p22 polypeptide Met-p22.

XX KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
XX KW hepatocyte; liver; Met-p22.

XX OS Hepatitis B virus.
OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Protein 2, 194
XX ET /label= p22

XX PN WO9809649-A1.

XX PD 12-MAR-1998.

XX PF 03-SEP-1997; 97WO-US15500.

XX PR 03-SEP-1996; 96US-0025370.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Melegari M, Scaglioni PP, Wands JR;

XX WPI; 1998-193325/17.

XX DNA encoding proteins which can be incorporated with wild type
PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
PT inhibition of viral replication, especially hepatitis B virus

XX PS Claim 11; Page 40; 60pp; English.

XX This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)
CC protein with an added N-terminal Met residue. p22 is produced by
CC elimination of the 19-amino acid leader peptide from the 25 kDa
CC full-length HBV precore protein (see AAW50250). Evidence is provided
CC that HBV replication is inhibited in the presence of high levels of
CC HBV precore or precore-related proteins. These proteins can be
CC incorporated into HBV nucleocapsids along with the p21 core protein
CC (see AAW50251), which is the usual nucleocapsid component, and
CC thereby render the nucleocapsids deficient in encapsitating HBV
CC pregenomic RNA. Thus, over-expression of the precore proteins, or
CC certain variants of them, leads to transdominant inhibition of HBV
CC replication. Suitable inhibitory proteins include p25 (see AAW50250),
CC p22, Met-p22, p18 (see AAW50236), Met-p18 (see AAW50237) and Met-p18-Het
CC (see AAW50238). Heterologous peptides (see AAW50244-49) may be
CC inserted into the p22 and Met-p22 polypeptides. The inhibitory
CC proteins can be produced by recombinant methods using claimed

CC expression vectors and host cells. They can be provided exogenously
CC to the target cells for use in inhibiting HBV replication.
CC Alternatively, a nucleic acid construct that directs overexpression
CC of an inhibitory protein in target cells is used for the gene
CC therapy of HBV infection.

XX SQ Sequence 194 AA;

Query Match 98.5%; Score 956; DB 19; Length 194;
Best Local Similarity 98.9%; Pred. No. 9.2e-95;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDIDPYKRGATVVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 12 MDIDPYKRGATVVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 71

OY 61 CWGELMTLATWVGVLNLEDPASRDLYVSYVNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120
Db 72 CWGELMTLATWVGVLNLEDPASRDLYVSYVNTNMGKFRQLLWFHISCLTFGTETVIEYLV 131

OY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSOSPRRRRSQSRE 180
Db 132 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSOSPRRRRSQSRE 191

OY 181 SOC 183
Db 192 SOC 194

RESULT 9

AAW50250
ID AAW50250 standard; Protein; 212 AA.

XX AC AAW50250;

XX DT 28-SEP-1998 (first entry)

XX DE Hepatitis B virus precore p25 polypeptide.

XX KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
XX KW hepatocyte; liver; p25 protein.

XX OS Hepatitis B virus.

XX PN WO9809649-A1.

XX PD 12-MAR-1998.

XX PF 03-SEP-1997; 97WO-US15500.

XX PR 03-SEP-1996; 96US-0025370.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Melegari M, Scaglioni PP, Wands JR;

XX WPI; 1998-193325/17.

XX DNA encoding proteins which can be incorporated with wild type
PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
PT inhibition of viral replication, especially hepatitis B virus

XX PS Claim 15; Page 35; 60pp; English.

XX This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25)
CC protein that is encoded by the full-length HBV precore gene.
CC Evidence is provided that HBV replication is inhibited in the
CC presence of high levels of HBV precore or precore-related proteins.
CC These proteins can be incorporated into HBV nucleocapsids along
CC with the p21 core protein (see AAW50251), which is the usual
CC nucleocapsid component, and thereby render the nucleocapsids
CC deficient in encapsitating HBV pregenomic RNA. Thus, over-
CC expression of the precore proteins, or certain variants of them,

CC leads to transdominant inhibition of HBV replication. Suitable
 CC inhibitory proteins include p25, p22 (see AAW50241), Met-p22 (see
 CC AAW50242), p18 (see AAW50236), Met-p18 (see AAW50237) and Met-p18-Het
 CC (see AAW50238). The inhibitory proteins can be produced by
 CC recombinant methods using claimed expression vectors and host
 CC cells. They can be provided exogenously to the target cells for
 CC use in inhibiting HBV replication. Alternatively, a nucleic acid
 CC construct that directs overexpression of an inhibitory protein in
 CC target cells is used for the gene therapy of HBV infection.

XX Sequence 212 AA;

Query Match 98.5%; Score 956; DB 19; Length 212;
 Best Local Similarity 98.9%; Pred. No. 1e-94;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
 QY 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFKQLLWFHISCLTFCGTETVIELV 120
 DB 90 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFKQLLWFHISCLTFCGTETVIELV 149
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 180
 DB 150 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 209
 QY 181 SQC 183
 DB 210 SQC 212

RESULT 10

AAE19793
 ID AAE19793 standard; Protein; 212 AA.

XX AAE19793;

DT 18-JUN-2002 (first entry)

DE Hepatitis B virus core antigenic protein (HBcAg).

KW Hepatitis B virus core antigen; HBcAg; prophylactic; viral hepatitis;
 KW therapeutic; vaccine; acquired immune deficiency syndrome; influenza;
 KW polio; herpes; rabies; AIDS; foot-and-mouth disease.

XX Hepatitis B virus.

OS Key Location/Qualifiers
 FH Peptide 1..29
 FT /label= Signal-peptide
 FT Protein 30..212
 FT /label= Mature_HBc_protein

PN WO200177158-A1.

PD 18-OCT-2001.

XX 09-APR-2001; 2001WO-GB01607.

XX 07-APR-2000; 2000EP-0107118.

XX (MEDE-) MEDEVA EURO LTD.

XX Gehin A, Gilbert R, Stuart D, Rowlands D;

XX WPI; 2002-239995/29.

XX N-PSDB; AAD31509.

XX Hepatitis B (HB) core antigen fusion proteins, useful as vaccines for
 PT the prophylactic or therapeutic treatment of humans or animals against
 PT e.g. HB virus, viral hepatitis, hepatitis C virus, influenza, or

PT foot-and-mouth disease

XX Disclosure; Page 24-25; 27pp; English.

XX The present invention relates to hepatitis B virus (HBV) core antigen
 CC (HBcAg) fusion proteins and polynucleotides encoding such proteins.
 CC Sequences of the invention are useful in methods of prophylactic or
 CC therapeutic vaccination or to manufacture medicaments for prophylactic
 CC or therapeutic vaccination of the human or animal body against HBV,
 CC e.g. against viral hepatitis. They are also useful as a prophylactic
 CC vaccine against e.g. hepatitis C virus, influenza, polio, herpes,
 CC rabies, acquired immune deficiency syndrome (AIDS) or foot-and-mouth
 CC disease. The present sequence is hepatitis B virus core antigenic
 CC protein (HBcAg).

SQ Sequence 212 AA;

Query Match 98.5%; Score 956; DB 23; Length 212;
 Best Local Similarity 98.9%; Pred. No. 1e-94;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
 QY 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFKQLLWFHISCLTFCGTETVIELV 120
 DB 90 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFKQLLWFHISCLTFCGTETVIELV 149
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 180
 DB 150 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 209
 QY 181 SQC 183
 DB 210 SQC 212

RESULT 11

AAE19898
 ID AAE19898 standard; Protein; 212 AA.

XX AAE19898;

DT 18-JUN-2002 (first entry)

XX Hepatitis B virus C antigen (HBcAg) and E antigen (HBeAg) sequence.

XX Hepatitis B virus; HBV; infection; virucide; fungicide; antibacterial;
 KW cytostatic; immunostimulant; vaccine; ribavirin; immune response; cancer.

OS Hepatitis B virus.

PN WO200213855-A2.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001WO-IB01808.

XX 17-AUG-2000; 2000US-225767P.

PR 29-AUG-2000; 2000US-229175P.

XX 03-NOV-2000; 2000US-0705547.

XX (TRIP-) TRIPEP AB.

XX Sallberg M, Hultgren C;

XX WPI; 2002-241837/29.

XX Vaccine compositions for treating and preventing disease, preferably
 PT hepatitis C virus infection, comprises ribavirin and antigen that has
 PT epitope present in hepatitis C virus

PS Claim 11; Page 82; 120pp; English.

XX The invention relates to a composition comprising ribavirin and an

CC antigen preferably non structural 3 protein (NS3)/4A fragment of

CC hepatitis C virus (HCV) genome or a peptide or nucleic acid of HCV

CC sequence. The composition is useful for enhancing an immune response to

CC a hepatitis C antigen in humans, domestic, sport or pet species and as

CC vaccines for treating and preventing HCV infections. The composition is

CC also useful for treating viral, bacterial, fungal diseases and cancer.

CC The present sequence is Hepatitis B virus C antigen (HBcAg) and E antigen

CC (HBeAg) sequence.

XX Sequence 212 AA;

SQ

Query Match 98.5%; Score 956; DB 23; Length 212;

Best Local Similarity 98.9%; Pred. No. 1e-94;

Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

DB 30 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

OY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGKFRQLLWFLHISCLTFGTETVIEYL 120

DB 90 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGKFRQLLWFLHISCLTFGTETVIEYL 149

OY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRPGSRPRRTSPRRRRSQSPRRRSQSRE 180

DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRRSQSRE 209

OY 181 SOC 183

DB 210 SOC 212

RESULT 12

AAEL7018

ID AAEL7018 standard; Protein; 212 AA.

XX AAEL7018;

XX 18-APR-2002 (first entry)

DE Hepatitis B virus (HBV) core antigen (HBcAg).

XX Hepatitis B virus; HBV; core antigen; HBcAg; immune system; typhoid;

KW prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes;

KW hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoea;

KW tuberculosis; polio; rabies; acquired immunodeficiency syndrome; AIDS;

KW dengue fever; yellow fever; malaria; whooping cough; salmonellosis;

KW food poisoning; meningitis; gonorrhea; antiviral; antibacterial;

KW antiprotozoal.

XX Hepatitis B virus.

OS

XX WO200198333-A2.

PN

XX 27-DEC-2001.

PD

XX 22-JUN-2001; 2001WO-GB02817.

PF

XX 22-JUN-2000; 2000GB-0015308.

PR

XX 06-OCT-2000; 2000GB-0024544.

XX (CELL-) CELTECH PHARM LTD.

PA

XX Page M, Li J, Pumpens P;

PI

XX WPI; 2002-098223/13.

XX N-PSDB; AAD27422.

DR

XX New proteins comprising a modified hepatitis B core antigen, useful as

PT a vaccine in prophylactic or therapeutic vaccination of the human or

PT animal body, particularly against hepatitis B virus infection -

XX Disclosure; Page 39-40; 40pp; English.

XX The invention relates to modified proteins comprising hepatitis B virus

CC (HBV) core antigen (HBcAg) wherein one or more of the four arginine

CC repeats has been deleted and the protein comprising the C-terminal

CC cysteine of HBcAg. The deleted region may be replaced by an epitope

CC from a protein other than HBcAg, in which case the HBcAg acts as a

CC carrier to present the epitope to the immune system. This chimeric

CC protein or its nucleic acid is useful as a vaccine or in a method of

CC prophylactic or therapeutic vaccination of the human or animal body,

CC particularly against HBV. The nucleic acid encoding the protein may

CC be used in gene therapy or DNA vaccination protocols. The chimeric

CC protein or its nucleic acid may also be used as the basis of a

CC prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis

CC A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth

CC disease, polio, herpes, rabies, acquired immunodeficiency syndrome

CC (AIDS), dengue fever, yellow fever, malaria, tuberculosis, whooping

CC cough, salmonellosis, typhoid, food poisoning, diarrhoea, meningitis

CC or gonorrhoea. The present sequence is Hepatitis B virus core antigen

CC (HBcAg).

XX Sequence 212 AA;

SQ

Query Match 98.5%; Score 956; DB 23; Length 212;

Best Local Similarity 98.9%; Pred. No. 1e-94;

Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

DB 30 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

OY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGKFRQLLWFLHISCLTFGTETVIEYL 120

DB 90 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGKFRQLLWFLHISCLTFGTETVIEYL 149

OY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRPGSRPRRTSPRRRRSQSPRRRSQSRE 180

DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRRSQSRE 209

OY 181 SOC 183

DB 210 SOC 212

RESULT 13

AAAR27473

ID AAAR27473 standard; Protein; 346 AA.

XX AAAR27473;

XX 25-MAR-2003 (updated)

DT 24-FEB-1993 (first entry)

XX S12/core protein.

XX Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;

KW vaccinia virus; 13L; promoter; NYVAC; recombinant; HBV L;

KW large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core;

KW S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;

KW deletion loci; recipient loci.

XX Synthetic.

OS

XX Key Location/Qualifiers

PH 1..108

FT region /label S1

FT region 109..163

FT /label= S2

FT region 164..346

FT /label= Core

XX

PN W09215672-A1.

XX 17-SEP-1992.

XX 09-MAR-1992; 92WO-US01906.

XX 07-MAR-1991; 91US-0666056.

PR 11-JUN-1991; 91US-0713967.

PR 06-MAR-1992; 92US-0847951.

XX (VIRO-) VIROGENETICS CORP.

XX Cox WI, De Taisne C, Francis J, Gettig RR, Johnson GP;

PI Limbach KJ, Norton EK, Paoletti E, Perkus ME, Pincus SE;

PI Riviere M, Tartaglia J, Taylor J;

XX WPI; 1992-331718/40.

DR N-PSDB; AAQ29105.

XX Vaccine comprises recombinant, attenuated pox-virus - use for

XX vaccinating against viral infections such as rabies, hepatitis B,

XX HIV, HSV, EBV, CMV, mumps etc.

XX Disclosure; Fig 13; 456pp; English.

XX The sequence given is encoded by an expression cassette which

XX comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/

XX core) which is precisely linked to the I3L promoter derived from

XX vaccinia virus. This DNA sequence was linked to the S1 and S2

XX sequences and this fragment was used in the construction of a NYVAC

XX recombinant expressing the HBV gene. Other HBV genes were also used

XX in the construction. These were HBV M protein (small pre-S antigen,

XX spsAg) and HBV L (large pre-S antigen, lpsAg). Each of these gene

XX sequences were inserted individually into three different sites of

XX NYVAC separated by from each other by large regions of vaccinia DNA

XX containing essential genes. NYVAC is a Copenhagen vaccine strain of

XX vaccinia virus which has been modified by deletion of six non-essential

XX regions of the genome encoding known or potential virulence factors.

XX The deletion loci were engineered as recipient loci for the insertion

XX of foreign genes. The spacing of the three inserted sequences ensured

XX that any recombination that did occur would lead to disruption of the

XX vaccinia genome and would cause unviable vaccinia virus. See also

XX AAQ35501-864.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 346 AA;

XX Query Match 98.5%; Score 956; DB 13; Length 346;

XX Best Local Similarity 98.9%; Pred. No. 1.9e-94;

XX Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRAIL 60

Db 164 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRAIL 223

QY 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTGTETVIEYLV 120

Db 224 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTGTETVIEYLV 283

QY 121 SFGVWIRTPPAYRPNAPILSTLPTTVRRGRSPRRRTSPRRRRSQSRRS 180

Db 284 SFGVWIRTPPAYRPNAPILSTLPTTVRRGRSPRRRTSPRRRRSQSRRS 343

QY 181 SQC 183

Db 344 SQC 346

RESULT 14

ABG94185

ID ABG94185 standard; Protein; 183 AA.

XX

AC ABG94185;

XX

DT

XX

DE

XX

KW

KW

KW

KW

OS

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PN

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PD

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XX

10-DEC-2002 (first entry)

Hepatitis B capsid (core) protein antigen (HBcAg) variant #14.

Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;

cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;

vaccine; infectious disease.

Hepatitis B virus.

WO200256905-A2.

25-JUL-2002.

21-JAN-2002; 2002WO-IB00166.

19-JAN-2001; 2001US-262379P.

04-MAY-2001; 2001US-288549P.

05-OCT-2001; 2001US-326998P.

07-NOV-2001; 2001US-331045P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.

Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;

Plossek C;

WPI; 2002-627351/67.

Molecular antigen array used in the production of vaccines for

infectious diseases -

Claim 112; Page 340; 441pp; English.

This invention relates to a novel ordered and repetitive antigen array used in the production of vaccines for infectious diseases. The invention also discloses a composition comprising a non-natural molecular scaffold comprising a core particle selected from a core particle of a non-natural origin and a core particle of natural origin and an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one covalent bond. Also disclosed is an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is amyloid beta peptide (Abeta1-42) or its fragment and where the second attachment site is selected from an attachment site not naturally occurring with the antigen or antigenic determinant and an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The invention also comprises a coat protein capable of forming a capsid which comprises mutant Qbeta coat proteins having an amino acid sequence selected from five amino acid sequences fully defined in the specification. The compounds of the invention may have antimicrobial, antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic, or hypoglycaemic activities and may be used in immunisation and as a vaccine. The present sequence represents a protein sequence used to create the compositions of the invention.

Sequence 183 AA;

Query Match 98.2%; Score 954; DB 23; Length 183;

Best Local Similarity 98.4%; Pred. No. 1.4e-94;

Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRAIL 60

Db 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRAIL 60

QY 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTGTETVIEYLV 120

Db 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTGTETVIEYLV 120

QY 121 SFGWIRTPPAYPPNAPILSTLPETVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
 |||||
 Db 121 SFGWIRTPPAYPPNAPILSTLPETVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
 |||||
 QY 181 SQC 183
 |||||
 Db 181 SQC 183

RESULT 15

ABG80497
 ID ABG80497 standard; Protein; 183 AA.

AC ABG80497;

XX 29-NOV-2002 (first entry)

DE Hepatitis B virus core capsid protein, HBcAg, variant #14.

XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.

XX Hepatitis B virus.

XX WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-IB00168.

XX 19-JAN-2001; 2001US-262379P.

XX 04-MAY-2001; 2001US-288549P.

XX 05-OCT-2001; 2001US-326998P.

XX 07-NOV-2001; 2001US-331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (NOVS) NOVARTIS PHARMA AG.

PA (MAUR/) MAURER P.

PA (LECH/) LECHNER F.

PA (ORTM/) ORTMANN R.

PA (LUBO/) LUBOEND R.

PA (STAU/) STAUFENBIEL M.

PA (FREY/) FREY P.

PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;

PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;

XX WPI; 2002-636514/68.

XX Molecular antigen array used in the production of vaccines for
 PT infectious diseases -

PS Claim 14; Page 317; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from:
 CC (1) a core particle of a non-natural origin; and (2) a core particle of
 CC natural origin; and (ii) an organiser comprising at least one first
 CC attachment site, where the organiser is connected to the core particle by
 CC at least one covalent bond; (b) an antigen or antigenic determinant with
 CC at least one second attachment site, where the antigen or antigenic
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and
 CC where the second attachment site is selected from: (i) an attachment site

CC not naturally occurring with the antigen or antigenic determinant; and
 CC (ii) an attachment site naturally occurring with the antigen or
 CC antigenic determinant, where the second attachment site is capable of
 CC association through at least one non-peptide bond to the first attachment
 CC site; and where the antigen or antigenic determinant and the scaffold
 CC interact through the association to form an ordered and repetitive
 CC antigen array. Also included is a process for producing a non-naturally
 CC occurring ordered and repetitive antigen array. The composition is used
 CC in immunisation and as a vaccine for diseases such as influenza,
 CC graft versus host disease, IgE-mediated allergic reactions, anaphylaxis,
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's
 CC disease, systemic lupus erythematosus, inflammatory immune diseases,
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's
 CC disease, osteoporosis and infectious diseases. The present sequence is
 CC an antigen for use in the array of the invention. The antigen is
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a
 CC cysteine- containing N- or C-terminal linker peptide which serves as the
 CC attachment point to a virus like particle or bacterial protein (the
 CC scaffold protein).

XX Sequence 183 AA;

Query Match 98.2%; Score 954; DB 23; Length 183;
 Best Local Similarity 98.4%; Pred. No. 1.4e-94;
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
 |||||

Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
 |||||

QY 61 CWGELMTLATWGVNLEDPASRDLYVYVNTNMGLKFRQLLWFHISCLTFGTETVLEYLV 120
 |||||

Db 61 CWGELMTLATWGVNLEDPASRDLYVYVNTNMGLKFRQLLWFHISCLTFGTETVLEYLV 120
 |||||

QY 121 SFGWIRTPPAYPPNAPILSTLPETVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
 |||||

Db 121 SFGWIRTPPAYPPNAPILSTLPETVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
 |||||

QY 181 SQC 183

Db 181 SQC 183

Search completed: August 6, 2003, 09:43:43

Job time : 85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2003, 09:40:39 ; Search time 93 Seconds
(without alignments)
507.781 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPYKEFGATVELLSFLP.....RRRRSQSPRRRRSQSRESQC 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	956	98.5	212	12	Q89656 hepatitis b
2	953	98.1	183	12	Q8VBF8 hepatitis b
3	953	98.1	183	12	Q89437 hepatitis b
4	953	98.1	183	12	Q68008 hepatitis b
5	953	98.1	212	12	Q67876 hepatitis b
6	953	98.1	212	12	Q68020 hepatitis b
7	953	98.1	212	12	Q89597 hepatitis b
8	951	97.9	212	12	O11884 hepatitis b
9	951	97.9	212	12	Q68025 hepatitis b
10	951	97.9	212	12	Q68068 hepatitis b
11	950	97.8	212	12	Q68070 hepatitis b
12	950	97.8	212	12	Q67984 hepatitis b
13	950	97.8	212	12	Q68032 hepatitis b
14	948	97.6	212	12	Q915Y7 hepatitis b
15	948	97.6	212	12	Q91SZ5 hepatitis b
16	948	97.6	212	12	Q91SZ2 hepatitis b

17	948	97.6	212	12	Q91717	Q91717 hepatitis b
18	948	97.6	212	12	Q91SX9	Q91SX9 hepatitis b
19	948	97.6	212	12	Q910K2	Q910K2 hepatitis b
20	947	97.5	183	12	Q910W2	Q910W2 hepatitis b
21	947	97.5	183	12	Q8VBF6	Q8VBF6 hepatitis b
22	947	97.5	183	12	Q68048	Q68048 hepatitis b
23	947	97.5	183	12	Q68066	Q68066 hepatitis b
24	947	97.5	212	12	Q67872	Q67872 hepatitis b
25	947	97.5	212	12	Q68051	Q68051 hepatitis b
26	946	97.4	183	12	Q67989	Q67989 hepatitis b
27	946	97.4	212	12	Q67980	Q67980 hepatitis b
28	946	97.4	212	12	Q91T01	Q91T01 hepatitis b
29	946	97.4	212	12	Q91SX4	Q91SX4 hepatitis b
30	946	97.4	212	12	Q68014	Q68014 hepatitis b
31	946	97.4	212	12	Q68012	Q68012 hepatitis b
32	945	97.3	183	12	Q8VBH0	Q8VBH0 hepatitis b
33	945	97.3	212	12	Q910N8	Q910N8 hepatitis b
34	945	97.3	212	12	Q910U3	Q910U3 hepatitis b
35	945	97.3	212	12	Q68077	Q68077 hepatitis b
36	945	97.3	212	12	Q68010	Q68010 hepatitis b
37	945	97.3	212	12	Q91SV4	Q91SV4 hepatitis b
38	945	97.3	212	12	Q91SZ1	Q91SZ1 hepatitis b
39	945	97.3	212	12	Q68075	Q68075 hepatitis b
40	944	97.2	183	12	Q8UYJ2	Q8UYJ2 hepatitis b
41	944	97.2	183	12	Q8UYA0	Q8UYA0 hepatitis b
42	944	97.2	212	12	Q68030	Q68030 hepatitis b
43	944	97.2	212	12	Q917J5	Q917J5 hepatitis b
44	944	97.2	212	12	Q9QMH8	Q9QMH8 hepatitis b
45	944	97.2	212	12	Q96845	Q96845 hepatitis b

ALIGNMENTS

RESULT 1

Q89656 PRELIMINARY; PRT; 212 AA.
AC Q89656;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Core antigen (Precore protein).
GN PREC.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AYW4;
RA Plucienniczak A.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012091; PubMed=399327;
RA Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw) cloned in E. coli.";
RL Nature 281:646-650(1979).
RN [4]
RP SEQUENCE FROM N.A.
RA Borisova G.P., Pumpen P.P., Bychko V.V., Pushko P.M., Kalis Y.V.,
RA Dishler A.V., Gren E.Y., Tsubinogin V.V., Kukain R.A.;
RL Dokl. Biochem. 279:386-390(1985).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RA Petzold D.R., Tautz B., Wolf F., Drescher J.;
RT "Infection chains and evolution rates of Hepatitis B Virus in cardiac transplant recipients infected nosocomially.";


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DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE HBCAG (PRE-CORE protein) (PRECORE/core protein).
OS Hepatitis B virus (subtype ayw), and
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418, 10407;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus (subtype ayw); STRAIN-SUB-TYPE AYW;
RX MEDLINE=94079539; PubMed=8257295;
RA Preisler-Adams S., Schlager M.J., Peters T., Hettler F., Gerok W.,
RA Pasenack J.;
RT "Sequence analysis of hepatitis B virus DNA in immunologically
RT negative infection.";
RL Arch. Virol. 133:385-396(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus (subtype ayw); STRAIN-AYW;
RA Karayiannis P.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus (subtype ayw); STRAIN-AYW;
RA Karayiannis P.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus; STRAIN=I43-Fam G;
RA Zampino R., Lobello S., Chiaramonte M., Venturi-Pasini C., Dumpis U.,
RA Thurez M., Karayiannis P.;
RT "Intra-familial transmission of Hepatitis B virus in Italy:
RT Phylogenetic sequence analysis and amino acid variation of the core
RT gene.";
RL J. Hepatol. 0:0-0(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus; STRAIN=Gam1119F29, and Gam1821P217;
RA Dumpis U., Mendy M., Karayiannis P.;
RT "Prevalence of HBV core promoter/precore/core mutations in Gambian
RT chronic carriers.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: X72702; CAA51257.1; -
DR EMBL: X80925; CAA56887.1; -
DR EMBL: AF419525; AAL15953.1; -
DR EMBL: AF350127; AAK57244.1; -
DR EMBL: AF350205; AAK57322.1; -
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1
RT CHAIN 30 212 CORE PROTEIN.
SEQUENCE 212 AA; 24336 MW; 1861B13E8B047AC8 CRC64;

Query Match 98.1%; Score 953; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 2.7e-89;
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120
DB 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
DB 210 SQC 212

RESULT 9
Q68025 PRELIMINARY; PRT; 212 AA.
AC Q68025;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Pre-c/core protein.
GN PRE-C/CORE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: X85293; CAA59616.1; -
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24363 MW; 6940D04E90A410C3 CRC64;

Query Match 97.9%; Score 951; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 4.3e-89;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120
DB 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
DB 210 SQC 212

RESULT 8
Q68025 PRELIMINARY; PRT; 212 AA.
AC Q68025;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Pre-c/core protein.
GN PRE-C/CORE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: X85293; CAA59616.1; -
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
SEQUENCE 212 AA; 24363 MW; 6940D04E90A410C3 CRC64;

Query Match 97.9%; Score 951; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 4.3e-89;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120
DB 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
DB 210 SQC 212

RESULT 8
```

RESULT 8

Db 90 CWGELMTLATWVGWNLDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 180
Db 150 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
Db 210 SQC 212

RESULT 10

Q68068 PRELIMINARY; PRT; 212 AA.
AC Q68068;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Pre-c/core protein.
GN PRE-C/CORE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85315; CAA59664.1; -
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24366 MW; CEABDD4E8B11E5E8 CRC64;

Query Match 97.9%; Score 951; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 4.3e-89;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGWNLDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
Db 90 CWGELMTLATWVGWNLDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 180
Db 150 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
Db 210 SQC 212

RESULT 11

Q68070 PRELIMINARY; PRT; 212 AA.
AC Q68070;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Pre-c/core protein.
GN PRE-C/CORE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85316; CAA59665.1; -
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24376 MW; D30173662996A1B8 CRC64;

Query Match 97.8%; Score 950; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 5.4e-89;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGWNLDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
Db 90 CWGELMTLATWVGWNLDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 180
Db 150 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
Db 210 SQC 212

RESULT 12

Q67984 PRELIMINARY; PRT; 212 AA.
AC Q67984;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Pre-c/core protein.
GN PRE-C/CORE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85256; CAA59519.1; -
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24322 MW; 629E0B298B13D0D1 CRC64;

Query Match 97.8%; Score 950; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 5.4e-89;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGWNLDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
Db 90 CWGELMTLATWVGWNLDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 180
Db 150 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
Db 210 SQC 212

RESULT 13

Q68032 PRELIMINARY; PRT; 212 AA.
AC Q68032;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Pre-c/core protein.
GN PRE-C/CORE.

OS Hepatitis B virus.
OC Viruses; Retrovirdae; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;
RN [1]

RP SEQUENCE FROM N.A.

RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; X85296; CAA59622.1; -;
DR InterPro: IPR002006; Hepatitis_core.

DR Pfam: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24308 MW; E28972C78B1604FF CRC64;

Query Match

Best Local Similarity 97.8%; Score 950; DB 12; Length 212;
Matches 179; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFWHISCLTFFGTETVIEYL 120
DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFWHISCLTFFGTETVIEYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSRRRSQSRE 180
DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSRRRSQSRE 209

QY 181 SQC 183
DB 210 SQC 212

RESULT 14

ID Q91SV7 PRELIMINARY; PRT; 212 AA.

AC Q91SV7;
DT 01-DEC-2001 (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)

DE Precore/core protein.

OS Hepatitis B virus.

OC Viruses; Retrovirdae; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;
RN [1]

RP SEQUENCE FROM N.A.

RA Dumpis U., Mendy M., Karayiannis P.;
RT "Prevalence of HBV core promoter/precure/core mutations in Gambian

chronic carriers";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF350155; AAK57272.1; -;
DR InterPro: IPR002006; Hepatitis_core.

DR Pfam: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24363 MW; 27E96F6D069BC35A CRC64;

Query Match

Best Local Similarity 97.8%; Score 948; DB 12; Length 212;
Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFWHISCLTFFGTETVIEYL 120
DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFWHISCLTFFGTETVIEYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSRRRSQSRE 180
DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSRRRSQSRE 209

QY 181 SQC 183
DB 210 SQC 212

RESULT 14

ID Q91SV7 PRELIMINARY; PRT; 212 AA.

AC Q91SV7;
DT 01-DEC-2001 (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)

DE Precore/core protein.

OS Hepatitis B virus.

OC Viruses; Retrovirdae; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;
RN [1]

RP SEQUENCE FROM N.A.

RA Dumpis U., Mendy M., Karayiannis P.;
RT "Prevalence of HBV core promoter/precure/core mutations in Gambian

chronic carriers";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF350155; AAK57272.1; -;
DR InterPro: IPR002006; Hepatitis_core.

DR Pfam: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24363 MW; 27E96F6D069BC35A CRC64;

Query Match

Best Local Similarity 97.8%; Score 948; DB 12; Length 212;
Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFWHISCLTFFGTETVIEYL 120
DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFWHISCLTFFGTETVIEYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSRRRSQSRE 180
DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSRRRSQSRE 209

QY 181 SQC 183
DB 210 SQC 212

RESULT 14

ID Q91SV7 PRELIMINARY; PRT; 212 AA.

AC Q91SV7;
DT 01-DEC-2001 (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)

DE Precore/core protein.

OS Hepatitis B virus.

OC Viruses; Retrovirdae; Hepadnaviridae; Orthohepadnavirus.

DB 210 SQC 212
|||

RESULT 15

Q91SZ5

ID Q91SZ5 PRELIMINARY; PRT; 212 AA.

AC Q91SZ5;
DT 01-DEC-2001 (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)

DE Precore/core protein.

OS Hepatitis B virus.

OC Viruses; Retrovirdae; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;
RN [1]

RP SEQUENCE FROM N.A.

RA Dumpis U., Mendy M., Karayiannis P.;
RT "Prevalence of HBV core promoter/precure/core mutations in Gambian

chronic carriers";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF350134; AAK57251.1; -;
DR InterPro: IPR002006; Hepatitis_core.

DR Pfam: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24363 MW; 9EF3ADC58CF9CB78 CRC64;

Query Match

Best Local Similarity 97.6%; Score 948; DB 12; Length 212;
Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFWHISCLTFFGTETVIEYL 120
DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFWHISCLTFFGTETVIEYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSRRRSQSRE 180
DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSRRRSQSRE 209

QY 181 SQC 183
DB 210 SQC 212

Search completed: August 6, 2003, 09:45:57
Job time : 96 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 6, 2003, 09:31:33 ; Search time 24 Seconds
(without alignments)
358.579 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPYKEGATVLLSFLP.....RRRSQSPRRRSQSRQ 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	956	98.5	183	1	CORA_HPBVY
2	937	96.5	183	1	CORA_HPBVZ
3	932	96.0	211	1	CORA_HPBVA
4	924	95.2	183	1	CORA_HPBVJ
5	924	95.2	183	1	CORA_HPBVO
6	924	95.2	185	1	CORA_HPBVM
7	923	95.1	183	1	CORA_HPBV4
8	916	94.3	185	1	CORA_HPBV2
9	908	93.5	214	1	CORA_HPBV9
10	906	93.3	195	1	CORA_HPBVF
11	904	93.1	183	1	CORA_HPBVL
12	901	92.8	212	1	CORA_HPBVT
13	672.5	69.3	188	1	CORA_HBV1
14	671	69.1	217	1	CORA_HPBGS
15	664	68.4	187	1	CORA_HBV8
16	173	17.8	305	1	CORA_HPBHE
17	154.5	15.9	305	1	CORA_HPBDC
18	152.5	15.7	305	1	CORA_HPBDB
19	151	15.6	305	1	CORA_HPBWD
20	149.5	15.4	305	1	CORA_HPBDO
21	97	10.0	196	1	SFR2_CAEEL
22	94.5	9.7	219	1	NOL3_HUMAN
23	90.5	9.3	208	1	YSX2_CAEEL
24	90.5	9.3	1007	1	PR4B_HUMAN
25	90.5	9.3	1007	1	PR4E_MOUSE
26	88	9.1	253	1	GH22_RAT
27	87.5	9.0	484	1	SFR2_HUMAN
28	87	9.0	3148	1	HD_FUGRU
29	83.5	8.6	1195	1	KCH7_MOUSE
30	83	8.5	253	1	GH22_MOUSE
31	83	8.5	306	1	RM45_MOUSE
32	80.5	8.3	955	1	T150_HUMAN
33	80.5	8.3	1195	1	KCH7_RAT

34 78.5 8.1 483 1 VE2_HPV14
35 78 8.0 503 1 VE2_HPV21
36 77.5 8.0 498 1 VE2_HPV08
37 77.5 8.0 3695 1 LMA5_HUMAN
38 77 7.9 576 1 CATA_RHOCA
39 76 7.8 164 1 SFR3_HUMAN
40 76 7.8 540 1 HXTD_YEAST
41 76 7.8 784 1 DPO2_AERPE
42 75.5 7.8 557 1 MK04_HUMAN
43 75.5 7.8 1048 1 SRA4_RAT
44 75.5 7.8 1874 1 POLR_KYMWJ
45 75 7.7 331 1 YOO1_CAEEL

ALIGNMENTS

RESULT 1
CORA_HPBVY ID CORA_HPBVY STANDARD; PRT; 183 AA.
AC P03146;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012091; PubMed=399327;
RA Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
cloned in E. coli.";
RL Nature 281:646-650(1979).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Latvia;
RX MEDLINE=85204397; PubMed=3996597;
RA Bichko V., Pushko P., Dreilina D., Pumpen P., Gren E.;
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
analysis.";
RL FEBS Lett. 185:208-212(1985).
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CC -----
EMBL; V01460; CAA24706.1; ALT_INIT.
DR EMBL; X02496; -; NOT_ANNOTATED_CDS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162..169
FT REPEAT 170..177
FT VARIANT 33..33 T -> N (IN STRAIN LATVIA).
FT VARIANT 80..80 A -> I (IN STRAIN LATVIA).
SQ SEQUENCE 183 AA; 21116 MW; E0D9D9763F24E958 CRC64;
Query Match 98.5%; Score 956; DB 1; Length 183;
Best Local Similarity 98.5%; Pred. No. 2.3e-80;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVLLSFLPSPDFPSVRDLDPFASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVLLSFLPSPDFPSVRDLDPFASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTATWGVNLEDPASRDVSVYVNTNMGKFRQLWFLHISCLTFGTETVIELV 120

Db 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSRRSRE 180
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSRRSRE 180

QY 181 SOC 183
 Db 181 SOC 183

RESULT 2

ID CORA_HPBVJ STANDARD; PRT; 183 AA.
 AC P03147;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1989 (Rel. 12, Last annotation update)
 DE Core antigen.

GN C.
 OS Hepatitis B virus (subtype adw).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10419;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=81012115; PubMed=399329;
 RA Pasek M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,
 RA Leadbetter G., Murray K., and their expression in E. coli.;
 RT "Hepatitis B virus genes and their expression in E. coli.";
 RL Nature 282:575-579(1979).

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DR EMBL: J02202; AAA45486.1;
 DR EMBL: A08967; CAA00816.1;
 DR PIR: B93217; NKVLAA2.
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT REPEAT 162 169
 FT REPEAT 170 177
 QY SEQUENCE 183 AA; 21042 MW; 545ED0E5527F26C CRC64;

Query Match 96.5%; Score 937; DB 1; Length 183;
 Best Local Similarity 95.6%; Pred. No. 1.3e-78;
 Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
 Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTAAALYRDALESEPHCSPHHTALRQAIL 60
 QY 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 120
 Db 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSRRSRE 180
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSRRSRE 180
 QY 181 SOC 183
 Db 181 SOC 183

RESULT 3

CORA_HPBVA

ID CORA_HPBVA STANDARD; PRT; 211 AA.
 AC P24023;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Core antigen.
 GN C.
 OS Hepatitis B virus (strain alpha).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10411;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90266476; PubMed=2345966;
 RA Tong S., Li J., Vitvitski L., Trepo C.;
 RT "Active hepatitis B virus replication in the presence of anti-HBe is
 RL associated with viral variants containing an inactive pre-C region.";
 RL Virology 176:596-603(1990).
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 CC -----
 DR EMBL: M32138; -: NOT_ANNOTATED_CDS.
 DR PIR: A34773; NKVLAL.
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT REPEAT 183 190
 FT REPEAT 198 206
 QY SEQUENCE 211 AA; 24208 MW; B774AC72E65C75AB CRC64;
 Query Match 96.0%; Score 932; DB 1; Length 211;
 Best Local Similarity 95.6%; Pred. No. 4.3e-78;
 Matches 175; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
 Db 29 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 88
 QY 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 120
 Db 89 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 148
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSRRSRE 180
 Db 149 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSRRSRE 208
 QY 181 SOC 183
 Db 209 SOC 211

RESULT 4
 ID CORA_HPBVJ STANDARD; PRT; 183 AA.
 AC P17391;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Core antigen.
 OS Hepatitis B virus (subtype adw / strain Japan/pJDN233).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RT "Typing hepatitis B virus by homology in nucleotide sequence:

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comparison of surface antigen subtypes.*;
J. Gen. Virol. 69:2575-2583(1988).
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-----
EMBL; D00329; ; NOT_ANNOTATED_CDS.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5F5AF5E160 CRC64;

Query Match 95.2%; Score 924; DB 1; Length 183;
Best Local Similarity 95.1%; Pred. No. 2e-77;
Matches 174; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFDPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFDPSPVRDLDTASALYREALKSPHCSPHHTALRQAIL 60
Qy 61 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKFRQLLWFHISCLTFCGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKIRQLLWFHISCLTFCGTETVIEYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGSPRRRTSPRRRSQSRRRSQSRE 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGSPRRRTSPRRRSQSRRRSQSRE 180
Qy 181 SQC 183
Db 181 SQC 183

RESULT 5
COR_A_HPBVO STANDARD; PRT; 183 AA.
AC P17392;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adv / strain Okinawa/pODW282).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
FT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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-----
EMBL; D00330; ; NOT_ANNOTATED_CDS.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169

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FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21081 MW; 66BDB2633122930C CRC64;

Query Match 95.2%; Score 924; DB 1; Length 183;
Best Local Similarity 95.1%; Pred. No. 2e-77;
Matches 174; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFDPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFDPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Qy 61 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKFRQLLWFHISCLTFCGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKIRQLLWFHISCLTFCGTETVIEYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGSPRRRTSPRRRSQSRRRSQSRE 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGSPRRRTSPRRRSQSRRRSQSRE 180
Qy 181 SQC 183
Db 181 SQC 183

RESULT 6
COR_A_HPBVO STANDARD; PRT; 185 AA.
AC P03149;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adv).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=106821;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adv.";
RL Nucleic Acids Res. 11:1747-1757(1983).
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-----
EMBL; V00866; ; NOT_ANNOTATED_CDS.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21394 MW; B86A90D541BA70F9 CRC64;

Query Match 95.2%; Score 924; DB 1; Length 185;
Best Local Similarity 95.1%; Pred. No. 2e-77;
Matches 176; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVELLSFDPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFDPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Qy 61 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKFRQLLWFHISCLTFCGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKIRQLLWFHISCLTFCGTETVIEYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRGSPRRRTSPRRRSQSRRRSQSRE 178

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Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
QY 179 RESQC 183
Db 181 RESQC 185

RESULT 7

CORA_HPBV4
ID CORA_HPBV4 STANDARD; PRT; 183 AA.
AC P03150; P03151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1990 (Rel. 01, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adr4),
OS Hepatitis B virus (subtype adr), and
OS Hepatitis B virus (subtype adr) / strain Indonesia/pIDW420).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409, 106820, 10412;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ADR;
RX MEDLINE=63168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
DNA; subtype adr and adr.";
RL Nucleic Acids Res. 11:1747-1757(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ADR4;
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyano H., Nozaki C., Yoneyama T., Ohtomo N.,
RA Matsubara K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
adr.";
RL Nucleic Acids Res. 11:4601-4610(1983).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ADR;
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
RN [4]
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RN [5]
RP EMBL; V00867; NOT ANNOTATED_CDS.
DR EMBL; X01587; CAA25745.1;
DR EMBL; D00331; NOT ANNOTATED_CDS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21095 MW; ED2DA1DB07FB596D CRC64;

Query Match 95.1%; Score 923; DB 1; Length 183;
Best Local Similarity 94.5%; Pred. No. 2.4e-77;
Matches 173; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
|||||

Db 1 MDIDPYKEFGASVELLSFLPSDFPSIRDLDTASALYREALSEPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWLFHISCLTFGRTVLEYLV 120
|||||
Db 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWLFHISCLTFGRTVLEYLV 120
|||||
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRRTSPRRRSQSPRRRSQSRE 180
|||||
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRRTSPRRRSQSPRRRSQSRE 180
|||||
QY 181 SOC 183
Db 181 SOC 183

RESULT 8

CORA_HPBV2
ID CORA_HPBV2 STANDARD; PRT; 185 AA.
AC P03148;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adr2).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (in) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21304 MW; 31F4DC338B507E19 CRC64;

Query Match 94.3%; Score 916; DB 1; Length 185;
Best Local Similarity 94.6%; Pred. No. 1.1e-76;
Matches 175; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
|||||
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
|||||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWLFHISCLTFGRTVLEYLV 120
|||||
Db 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWLFHISCLTFGRTVLEYLV 120
|||||
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRR--PGRSPRRRTSPRRRSQSPRRRSQS 178
|||||
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
|||||
QY 179 RESQC 183
Db 181 RESQC 185

RESULT 9

CORA_HPBV9
ID CORA_HPBV9 STANDARD; PRT; 214 AA.
AC P17099;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adr / strain 991).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]

```

RP SEQUENCE FROM N.A.
RA Koechel H.G., Schueler A., Lottmann S., Thomssen R.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X51970; CAA36232.1; -
DR PIR; S10381; NKVLKS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA; 24722 MW; 2D668333EC5AFB8C CRC64;

Query Match 93.5%; Score 908; DB 1; Length 214;
Best Local Similarity 94.6%; Pred. No. 6.7e-76;
Matches 175; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGLKFRQLLWFHISCLTFTGTVIEYLV 120
DB 90 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGLKIRQLLWFHISCLTFTGTVIEYLV 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQS 178
DB 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQS 209
QY 179 RESQC 183
DB 210 RESQC 214

RESULT 10
CORA_HPBVF STANDARD; PRT; 195 AA.
AC P29178;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adv2 variant sf).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169850; PubMed=2307406;
RA Bhat R.A., Ulrich P.P., Vyas G.N.;
RT "Molecular characterization of a new variant of hepatitis B virus in
RT a persistently infected homosexual man.";
RL Hepatology 11:271-276(1990).
DR PIR; A37182; NKVLH3.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 174 181
FT REPEAT 182 189
SQ SEQUENCE 195 AA; 22461 MW; E2B166F79CB7CB7 CRC64;

Query Match 93.3%; Score 906; DB 1; Length 195;
Best Local Similarity 93.4%; Pred. No. 9.2e-76;
Matches 171; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 13 LDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYRESLESDDHSCPHHTALRQAIL 72
QY 61 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGLKFRQLLWFHISCLTFTGTVIEYLV 120
DB 73 CWELMTLATWGVNLEDPASRDVLVSVYVNTNMGLKIRQLLWFHISCLTFTGTVIEYLV 132
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQS 180
DB 133 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQS 192
QY 181 SQC 183
DB 193 SQC 195

RESULT 11
CORA_HPBVL STANDARD; PRT; 183 AA.
AC P12901;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258473; PubMed=2838576;
RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
RA Harrison F.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee.";
RL J. Gen. Virol. 69:1383-1389(1988).
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CC -----
DR EMBL; D00220; BAA00157.1; -
DR PIR; A28885; NKVLCP.
DR PDB; 1HHH; 31-OCT-93.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat; 3D-structure.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 20959 MW; 923DCB94A33FC0E8 CRC64;

Query Match 93.1%; Score 904; DB 1; Length 183;
Best Local Similarity 93.4%; Pred. No. 1.3e-75;
Matches 171; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGLKFRQLLWFHISCLTFTGTVIEYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGLKIRQLLWFHISCLTFTGTVIEYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQS 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQS 180
QY 181 SQC 183

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Db 181 SQSPSANC 188

RESULT 14
CORR_HPBGS STANDARD; PRT; 217 AA.
AC P03153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE Core antigen.
GN C.
OS Ground squirrel hepatitis virus (GSV).
OX Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10406;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=84267998; PubMed=6086950;
RA Seeger C., Ganem D., Varmus H.E.;
RT "Nucleotide sequence of an infectious molecularly cloned genome of
ground squirrel hepatitis virus.";
RL J. Virol. 51:367-375(1984).
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DR EMBL; K02715; AAA46755.1; -
DR PIR; A03715; NKVLS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 196 203
FT REPEAT 204 211
SQ SEQUENCE 217 AA; 25189 MW; D489467355EC11A CRC64;
Query Match 69.1%; Score 671; DB 1; Length 217;
Best Local Similarity 67.6%; Pred. No. 2.9e-54;
Matches 127; Conservative 18; Mismatches 37; Indels 6; Gaps 2;
QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
DB 31 MDIDPYKEFGSSYQLLNFLPLDFFPDNLAVDTATAYEELTGREHCHSPHHTAIRQALV 90
QY 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLLWFHISCLTFGTETVIELV 120
DB 91 CWEELTRLITWMSNTTEEVRR-IIVDHVNTWGLKVRQTLWFLHLSCLTFGQHTVQEFV 149
QY 121 SFGVWIRTPPAYRPNAPILSTLPTETTVVRPG-----RSPRRTPSPRRRSQSPRRR 175
DB 150 SFGVWIRTPPAYRPNAPILSTLPTETTVVRPG-----RSPRRTPSPRRRSQSPRRR 175
QY 176 SQSRESQC 183
DB 210 SQSPASNC 217

RESULT 15
CORR_HVH8 STANDARD; PRT; 187 AA.
AC P06433;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE Core antigen.
GN C.
OS Woodchuck hepatitis virus 8 (WHV 8).
OX Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10433;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86062931; PubMed=3855246;
RA Kodama K., Ogasawara N., Yoshikawa H., Murakami S.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
evolutional relationship between hepadnaviruses.";
RL J. Virol. 56:978-986(1985).
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CC -----
DR EMBL; M11082; AAA19185.1; -
DR PIR; A03714; NKVLC2.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 166 173
FT REPEAT 174 181
SQ SEQUENCE 187 AA; D4BC446FF7163165 CRC64;
Query Match 68.4%; Score 664; DB 1; Length 187;
Best Local Similarity 66.3%; Pred. No. 1.1e-53;
Matches 124; Conservative 20; Mismatches 39; Indels 4; Gaps 1;
QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
DB 1 MDIDPYKEFGSSYQLLNFLPLDFFPDNLAVDTATAYEELTGREHCHSPHHTAIRQALV 60
QY 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLLWFHISCLTFGTETVIELV 120
DB 61 CWDELTKLIAMWSSNITSEQVRTIIVNHVNDTWGLKVRQSLWFLHLSCLTFGQHTVQEFV 120
QY 121 SFGVWIRTPPAYRPNAPILSTLPTETTVVRPG-----RSPRRTPSPRRRSQSPRRR 176
DB 121 SFGVWIRTPPAYRPNAPILSTLPTETTVVRPG-----RSPRRTPSPRRRSQSPRRR 180
QY 177 QSRESQC 183
DB 181 QSPSANC 187

Search completed: August 6, 2003, 09:44:15
Job time : 26 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 6, 2003, 09:41:04 ; Search time 40 Seconds
(without alignments)
439.972 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPYKEGATVLLSLP.....RRRRSQSPRRRRSQSRESQC 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956	98.5	212	1	NKVLAH
2	953	98.1	212	2	S53211
3	953	98.1	212	2	S32204
4	953	98.1	212	2	S20750
5	951	97.9	212	2	S53216
6	951	97.9	212	2	S53272
7	950	97.8	212	2	S53225
8	950	97.8	212	2	S53274
9	950	97.8	212	2	S53163
10	947	97.5	183	2	S53247
11	947	97.5	183	2	S53270
12	947	97.5	212	2	S53251
13	947	97.5	212	2	S20746
14	946	97.4	183	2	S53169
15	946	97.4	212	2	S53159
16	946	97.4	212	2	S53200
17	946	97.4	212	2	S53202
18	945	97.3	212	2	S53281
19	945	97.3	212	2	S53198
20	944	97.2	212	2	S53223
21	944	97.2	212	2	S53227
22	941	96.9	212	2	S53253
23	941	96.9	212	2	S53204
24	939	96.7	183	2	S53260
25	939	96.7	212	1	NKVLH
26	938	96.6	212	2	S53240
27	937	96.5	183	1	NKVLH2
28	937	96.5	183	2	S53181
29	936	96.4	212	2	S53242

ALIGNMENTS

RESULT 1

NKVLAH

e antigen precursor / core antigen - hepatitis B virus (subtype ayw4, isolate hb321 a)
N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw4, isolate hb321; isolate patient Ferracuti'83; isolate patient Cheri'83

C:Date: 18-Dec-1981 #sequence_revision 08-Nov-1996 #text_change 16-Jul-1999
C:Accession: S47405; S53191; S53209; S53234; S53264; S53249; S53262; S53277; A03711
R:Plucieniczak, A.
submitted to the EMBL Data Library, August 1994

A:Description: Molecular cloning and sequencing of two complete genomes of polish iso
A:Reference number: S47404
A:Accession: S47405
A:Molecule type: DNA

A:Residues: 1-212 <PIU>
A:Cross-references: EMBL:Z35716; NID:q527435; PIDN:CAA84786.1; PID:q527437
A:Experimental source: subtype ayw4, isolate hb321

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995

A:Reference number: S53112
A:Accession: S53191
A:Molecule type: DNA

A:Residues: 1-212 <LA1>
A:Cross-references: EMBL:X85283; NID:q736088; PIDN:CAA59593.1; PID:q736090
A:Experimental source: isolate patient Ferracuti'83

A:Accession: S53209
A:Molecule type: DNA
A:Residues: 1-212 <LA2>

A:Cross-references: EMBL:X85290; NID:q736114; PIDN:CAA59609.1; PID:q736116
A:Experimental source: isolate patient Castag'83

A:Accession: S53234
A:Molecule type: DNA
A:Residues: 1-212 <LA3>

A:Cross-references: EMBL:X85300; NID:q736150; PIDN:CAA59631.1; PID:q736152
A:Experimental source: isolate patient Sanna '84

A:Accession: S53264
A:Molecule type: DNA
A:Residues: 1-212 <LA4>

A:Cross-references: EMBL:X85313; NID:q736194; PIDN:CAA59659.1; PID:q736196
A:Experimental source: isolate patient Licheri-1'85

A:Accession: S53249
A:Molecule type: DNA
A:Residues: 1-212 <LA5>

A:Cross-references: EMBL:X85306; NID:q736172; PIDN:CAA59644.1; PID:q736174
A:Experimental source: isolate patient Fiore-1'86

A:Accession: S53262
A:Molecule type: DNA
A:Residues: 1-212 <LA6>

A:Cross-references: EMBL:X85312; NID:q736191; PIDN:CAA59657.1; PID:q736193
A:Experimental source: isolate patient Licheri'83

A:Accession: S53277
 A:Molecule type: DNA
 A:Residues: 30-212 <LAI>
 A:Cross-references: EMBL:X85317; NID:g736211; PIDN:CAA59669.1; PID:g736214.
 A:Experimental source: patient Giordo-2'86
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor
 R:Galibert, F.; Mandart, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.
 Nature 281, 646-650, 1979
 A:Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.
 A:Reference number: A93214; MUID:81012091; PMID:399327
 A:Accession: A03711
 A:Molecule type: DNA
 A:Residues: 1-212 <GAL>
 A:Cross-references: GB:J02203; NID:g329640; PIDN:AAA45489.1; PID:g329642
 A:Experimental source: subtype ayw
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-212/Product: core antigen #status predicted <CAG>
 F:30-178/Product: e antigen #status predicted <EAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <EC>

Query Match 98.5%; Score 956; DB 1; Length 212;
 Best Local Similarity 98.9%; Pred. No. 1.3e-76;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
 DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89
 QY 61 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIEYL 120
 DB 90 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIEYL 149
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTPSPRRRSQSPRRRSQSRE 180
 DB 150 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTPSPRRRSQSPRRRSQSRE 209
 QY 181 SQC 183
 DB 210 SQC 212

RESULT 2
 S53211
 e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag-1'85 and
 Alternate names: HBC antigen; HBe antigen precursor / HBC antigen; pre-C/C antigen
 Contains: core antigen; e antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Castag-1'85; isolate patient Ferracuti-1'89
 C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C:Accession: S53211; S53197
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53211
 A:Molecule type: DNA
 A:Residues: 1-212 <LAI>
 A:Cross-references: EMBL:X85291; NID:g736117; PIDN:CAA59611.1; PID:g736119
 A:Experimental source: isolate patient Castag-1'85
 A:Accession: S53197
 A:Molecule type: DNA
 A:Residues: 30-212 <LAW>
 A:Cross-references: EMBL:X85284; NID:g736095; PIDN:CAA59596.1; PID:g736098
 A:Experimental source: isolate patient Ferracuti-1'89
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>
 F:30-178/Product: e antigen #status predicted <EAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <EC>
 Query Match 98.1%; Score 953; DB 2; Length 212;
 Best Local Similarity 98.4%; Pred. No. 2.4e-76;
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
 DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89
 QY 61 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIEYL 120
 DB 90 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIEYL 149
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTPSPRRRSQSPRRRSQSRE 180
 DB 150 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTPSPRRRSQSPRRRSQSRE 209
 QY 181 SQC 183
 DB 210 SQC 212

RESULT 3
 S32204
 e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patients C1000 a
 Alternate names: HBe antigen precursor / HBC antigen; pre-C/C antigen
 N:Contains: core antigen; e antigen
 C:Species: hepatitis B virus, HBV
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Oct-2000
 C:Accession: S32204; S53207
 R:Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Rasenack, J.
 submitted to the EMBL Data Library, March 1993
 A:Description: Identification and sequence analysis of hepatitis B virus DNA in immun
 A:Reference number: S32202
 A:Accession: S32204
 A:Molecule type: DNA
 A:Residues: 1-212 <PR>
 A:Cross-references: EMBL:X72702; NID:g288927; PIDN:CAA51257.1; PID:g288930
 A:Experimental source: subtype ayw, patient C1000
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53207
 A:Molecule type: DNA
 A:Residues: 30-212 <LAI>
 A:Cross-references: EMBL:X85289; NID:g736110; PIDN:CAA59607.1; PID:g736113
 A:Experimental source: isolate patient Castaa-2'87
 A:Note: due to a stop codon mutation between the alternative initiators the e antigen
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-212/Product: core antigen #status predicted <CAG>
 F:30-178/Product: e antigen #status predicted <EAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <EC>

Query Match 98.1%; Score 953; DB 2; Length 212;
 Best Local Similarity 98.4%; Pred. No. 2.4e-76;
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
 DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89
 QY 61 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIEYL 120
 DB 90 CWGELMTLATWGVNLEDPASRDLYSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIEYL 149
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTPSPRRRSQSPRRRSQSRE 180

Db 150 SFGVWIRTPPAYRPPNAPILLSTLPTTAVRRGRSPRRTPSPRRRSQSRRRSQSRE 209
181 SQC 183
210 SQC 212

RESULT 4

S20750 e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patient CI)

N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N:Contains: core antigen; e antigen

C:Species: hepatitis B virus, HBV

A:Variety: subtype ayw, patient CI

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S20750

R:Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.

submitted to the EMBL Data Library, March 1992

Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative

A:Reference number: S20745

A:Accession: S20750

A:Molecule type: DNA

A:Residues: 1-212 <LAI>

A:Cross-references: EMBL:X65258; NID:g59434; PIDN:CAA46354.1; PID:g59436

A:Experimental source: subtype ayw, patient CI

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 98.1%; Score 953; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 2.4e-76;
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSVDRDLDTASALYREALSPHCHSPHHTALQAIL 60

Db 30 MDIDPYKEFGATVLLSFLPSVDRDLDTASALYREALSPHCHSPHHTALQAIL 89

Qy 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120

Db 90 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 149

Qy 121 SFGVWIRTPPAYRPPNAPILLSTLPTTAVRRGRSPRRTPSPRRRSQSRRRSQSRE 180

Db 150 AFGVWIRTPPAYRPPNAPILLSTLPTTAVRRGRSPRRTPSPRRRSQSRRRSQSRE 209

Qy 181 SQC 183

Db 210 SQC 212

RESULT 5

S53216 e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag'3)

N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N:Contains: core antigen; e antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Castag'3

C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C:Accession: S53216

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53216

A:Molecule type: DNA

A:Residues: 1-212 <LAI>

A:Cross-references: EMBL:X85293; NID:g736124; PIDN:CAA59616.1; PID:g736126

A:Experimental source: isolate patient Castag'3

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.9%; Score 951; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 3.6e-76;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSVDRDLDTASALYREALSPHCHSPHHTALQAIL 60

Db 30 MDIDPYKEFGATVLLSFLPSVDRDLDTASALYREALSPHCHSPHHTALQAIL 89

Qy 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120

Db 90 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 149

Qy 121 SFGVWIRTPPAYRPPNAPILLSTLPTTAVRRGRSPRRTPSPRRRSQSRRRSQSRE 180

Db 150 SFGVWIRTPPAYRPPNAPILLSTLPTTAVRRGRSPRRTPSPRRRSQSRRRSQSRE 209

Qy 181 SQC 183

Db 210 SQC 212

RESULT 6

S53272 e antigen precursor / core antigen - hepatitis B virus (isolate patient Licheri-3'90)

N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen

N:Contains: core antigen; e antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Licheri-3'90

C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C:Accession: S53272

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53272

A:Molecule type: DNA

A:Residues: 1-212 <LAI>

A:Cross-references: EMBL:X85315; NID:g736205; PIDN:CAA59664.1; PID:g736207

A:Experimental source: isolate patient Licheri-3'90

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.9%; Score 951; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 3.6e-76;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSVDRDLDTASALYREALSPHCHSPHHTALQAIL 60

Db 30 MDIDPYKEFGATVLLSFLPSVDRDLDTASALYREALSPHCHSPHHTALQAIL 89

Qy 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120

Db 90 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 149

Qy 121 SFGVWIRTPPAYRPPNAPILLSTLPTTAVRRGRSPRRTPSPRRRSQSRRRSQSRE 180

Db 150 SFGVWIRTPPAYRPPNAPILLSTLPTTAVRRGRSPRRTPSPRRRSQSRRRSQSRE 209

Qy 181 SQC 183

Db 210 SOC 212

RESULT 7

S53225
e antigen precursor / core antigen - hepatitis B virus (isolate patient Chighine-2'86)
N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Chighine-2'86
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53225
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53225
A:Molecule type: DNA
A:Residues: 1-212 <LAI>
A:Cross-references: EMBL:X85296; NID:g736137; PIDN:CAA59622.1; PID:g736139
A:Experimental source: isolate patient Chighine-2'86
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.8%; Score 950; DB 2; Length 212;

Best Local Similarity 97.8%; Pred. No. 4.4e-76;

Matches 179; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPKFEGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPKFEGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGTETVIELV 120
Db 90 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGTETVIELV 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SOC 183
Db 210 SOC 212

RESULT 8

S53274
e antigen precursor / core antigen - hepatitis B virus (isolate patient Giordo'84)
N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Giordo'84
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53274
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53274
A:Molecule type: DNA
A:Residues: 1-212 <LAI>
A:Cross-references: EMBL:X85316; NID:g736208; PIDN:CAA59666.1; PID:g736210
A:Experimental source: isolate patient Giordo'84
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.8%; Score 950; DB 2; Length 212;

Best Local Similarity 98.4%; Pred. No. 4.4e-76;

Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPKFEGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPKFEGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGTETVIELV 120
Db 90 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGTETVIELV 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SOC 183
Db 210 SOC 212

RESULT 9

S53163
e antigen precursor / core antigen - hepatitis B virus (isolate patient Vittorina'92)
N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Vittorina'92
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53163
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53163
A:Molecule type: DNA
A:Residues: 1-212 <LAI>
A:Cross-references: EMBL:X85256; NID:g736050; PIDN:CAA59519.1; PID:g736052
A:Experimental source: isolate patient Vittorina'92
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.8%; Score 950; DB 2; Length 212;

Best Local Similarity 98.4%; Pred. No. 4.4e-76;

Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPKFEGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPKFEGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGTETVIELV 120
Db 90 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGTETVIELV 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SOC 183
Db 210 SOC 212

RESULT 10

S53247
 core antigen - hepatitis B virus (isolate patient Flore-2'91)
 N:Alternate names: Hbc antigen
 N:Contains: core antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient patient Flore-2'91
 C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C:Accession: S53247
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53247
 A:Molecule type: DNA
 A:Residues: 1-183 <LAI>
 A:Cross-references: EMBL:X85305; NID:g736168; PIDN:CAA59642.1; PID:g736171
 A:Experimental source: isolate patient patient Flore-2'91
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 97.5%; Score 947; DB 2; Length 183;
 Best Local Similarity 97.8%; Pred. No. 6.9e-76;
 Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
 |||||
 Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
 |||||

Qy 61 CWGELMTLATWVGYNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 120
 |||||
 Db 61 CWGELMTLATWVGYNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 120
 |||||

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSRE 180
 |||||
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRGRSPRRRTSPRRRSQSPRRRSQSRE 180
 |||||

Qy 181 SQC 183
 ||||
 Db 181 SQC 183

RESULT 11
 S53270
 core antigen - hepatitis B virus (isolate patient Licheri-2'87)
 N:Alternate names: Hbc antigen
 N:Contains: core antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Licheri-2'87
 C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C:Accession: S53270
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53270
 A:Molecule type: DNA
 A:Residues: 1-183 <LAI>
 A:Cross-references: EMBL:X85314; NID:g736201; PIDN:CAA59662.1; PID:g736204
 A:Experimental source: isolate patient Licheri-2'87
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 97.5%; Score 947; DB 2; Length 183;
 Best Local Similarity 97.3%; Pred. No. 6.9e-76;
 Matches 178; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
 |||||
 Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
 |||||

Qy 61 CWGELMTLATWVGYNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 120
 |||||
 Db 61 CWGELMTLATWVGYNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 120
 |||||

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSRE 180
 |||||
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRGRSPRRRTSPRRRSQSPRRRSQSRE 180
 |||||

Qy 181 SQC 183
 ||||
 Db 181 SQC 183

RESULT 12
 S53251
 e antigen precursor / core antigen - hepatitis B virus (isolate patient Flore'85)
 N:Alternate names: Hbc antigen precursor / Hbc antigen; pre-C/C antigen
 N:Contains: core antigen; e antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Flore'85
 C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C:Accession: S53251
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53251
 A:Molecule type: DNA
 A:Residues: 1-212 <LAI>
 A:Cross-references: EMBL:X85307; NID:g736175; PIDN:CAA59646.1; PID:g736177
 A:Experimental source: isolate patient Flore'85
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-212/Product: core antigen #status predicted <CAG>
 F:30-178/Product: e antigen #status predicted <EAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.5%; Score 947; DB 2; Length 212;
 Best Local Similarity 97.8%; Pred. No. 8.1e-76;
 Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
 |||||
 Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89
 |||||

Qy 61 CWGELMTLATWVGYNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 120
 |||||
 Db 90 CWGELMTLATWVGYNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 149
 |||||

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSRE 180
 |||||
 Db 150 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRGRSPRRRTSPRRRSQSPRRRSQSRE 209
 |||||

Qy 181 SQC 183
 ||||
 Db 210 SQC 212

RESULT 13
 S20746
 e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patient C)
 N:Alternate names: Hbc antigen precursor / Hbc antigen; pre-C/C antigen
 N:Contains: core antigen; e antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: subtype ayw, patient C
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S20746
 R:Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.
 submitted to the EMBL Data Library, March 1992
 A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg neg

A:Reference number: S20745

A:Accession: S20746

A:Molecule type: DNA

A:Residues: 1-212 <LAI>

A:Cross-references: EMBL:X65257; NID:g59429; PIDN:CAA46350.1; PID:g59431

A:Experimental source: subtype ayw, patient C

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.5%; Score 947; DB 2; Length 212;

Best Local Similarity 97.8%; Pred. No. 8.1e-76;

Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

DB 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

DB 90 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180

DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 209

QY 181 SOC 183

DB 210 SOC 212

RESULT 14

S53169

core antigen - hepatitis B virus (isolate patient Muresu/89)

N:Alternate names: HBC antigen

N:Contains: core antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Muresu/89

C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C:Accession: S53169

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53169

A:Molecule type: DNA

A:Residues: 1-183 <LAI>

A:Cross-references: EMBL:X85275; NID:g736057; PIDN:CAA59571.1; PID:g736060

A:Experimental source: isolate patient Muresu/89

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

Query Match

Best Local Similarity 97.4%; Score 946; DB 2; Length 183;

Matches 178; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

DB 61 CWGELMTLATWGANLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180

DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180

Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180

QY 181 SOC 183

DB 181 SOC 183

Db 181 SOC 183

RESULT 15

S53159

e antigen precursor / core antigen - hepatitis B virus (isolate patient Garrucciu/90)

N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

N:Contains: core antigen; e antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Garrucciu/90

C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C:Accession: S53159

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53159

A:Molecule type: DNA

A:Residues: 1-212 <LAI>

A:Cross-references: EMBL:X85272; NID:g736044; PIDN:CAA59563.1; PID:g736046

A:Experimental source: isolate patient Garrucciu/90

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match

Best Local Similarity 97.4%; Score 946; DB 2; Length 212;

Matches 178; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

DB 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

DB 90 CWGELMTLATWGVNLEDPATRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180

DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 209

QY 181 SOC 183

DB 210 SOC 212

Search completed: August 6, 2003, 09:46:41

Job time : 40 secs

TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-812-862-12

Query Match 100.0%; Score 971; DB 9; Length 183;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
QY 61 CWGELMTLATWVGVLNEDPASRDVSVYNTNMGKLFROLLWFWHISCLTFFGTETVIEYLV 120
DB 61 CWGELMTLATWVGVLNEDPASRDVSVYNTNMGKLFROLLWFWHISCLTFFGTETVIEYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRRE 180
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRRE 180
QY 181 SOC 183
DB 181 SOC 183

RESULT 2

US-08-785-997-38
Sequence 38, Application US/08785997
Publication No. US20030021804A1
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process for Increasing
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-785-997-38

Query Match 98.5%; Score 956; DB 8; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.5e-86;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
QY 61 CWGELMTLATWVGVLNEDPASRDVSVYNTNMGKLFROLLWFWHISCLTFFGTETVIEYLV 120
DB 61 CWGELMTLATWVGVLNEDPASRDVSVYNTNMGKLFROLLWFWHISCLTFFGTETVIEYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRRE 180
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRRE 180
QY 181 SOC 183
DB 181 SOC 183

RESULT 3

US-09-387-340-38
Sequence 38, Application US/09387340
Publication No. US20030026808A1
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
APPLICANT: Gamson, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,340
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-387-340-38

Query Match 98.5%; Score 956; DB 11; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.5e-86;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60

QY 61 CWGELMTLATWGVGNLEDPASRDVLVSVYNTNMGKFRQLLWFIHISCLTGTETVIEYLV 120
Db 61 CWGELMTLATWGVGNLEDPASRDVLVSVYNTNMGKFRQLLWFIHISCLTGTETVIEYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTVTVRRGSRPRRTTSPRRRSQSPRRRSQSRE 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTVTVRRGSRPRRTTSPRRRSQSPRRRSQSRE 180
QY 181 SOC 183
Db 181 SOC 183

RESULT 4

US-09-848-616-99
; Sequence 99, Application US/09848616
; Publication No. US20030034010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-848-616-99

Query Match 98.5%; Score 956; DB 11; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.5e-86;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVLLSFPSDFPSVDRDLDTASALYREALSPHCSPHHTALROAIL 60
Db 1 MDIDPYKEFGATVLLSFPSDFPSVDRDLDTASALYREALSPHCSPHHTALROAIL 60
QY 61 CWGELMTLATWGVGNLEDPASRDVLVSVYNTNMGKFRQLLWFIHISCLTGTETVIEYLV 120
Db 61 CWGELMTLATWGVGNLEDPASRDVLVSVYNTNMGKFRQLLWFIHISCLTGTETVIEYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTVTVRRGSRPRRTTSPRRRSQSPRRRSQSRE 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTVTVRRGSRPRRTTSPRRRSQSPRRRSQSRE 180
QY 181 SOC 183
Db 181 SOC 183

RESULT 5

US-09-931-325A-170
; Sequence 170, Application US/09931325A
; Publication No. US20030034337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931,325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGNED
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 170

; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-931-325A-170
Query Match 98.5%; Score 956; DB 11; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.5e-86;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFPSDFPSVDRDLDTASALYREALSPHCSPHHTALROAIL 60
Db 1 MDIDPYKEFGATVLLSFPSDFPSVDRDLDTASALYREALSPHCSPHHTALROAIL 60
QY 61 CWGELMTLATWGVGNLEDPASRDVLVSVYNTNMGKFRQLLWFIHISCLTGTETVIEYLV 120
Db 61 CWGELMTLATWGVGNLEDPASRDVLVSVYNTNMGKFRQLLWFIHISCLTGTETVIEYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTVTVRRGSRPRRTTSPRRRSQSPRRRSQSRE 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTVTVRRGSRPRRTTSPRRRSQSPRRRSQSRE 180
QY 181 SOC 183
Db 181 SOC 183

RESULT 6

US-09-386-591-38
; Sequence 38, Application US/09386591
; Publication No. US20030100520A1
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: For Increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/386,591
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-386-591-38

Query Match 98.5%; Score 956; DB 11; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.5e-86;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKFGATVALLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKFGATVALLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFQLLWFHISCLTFGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFQLLWFHISCLTFGTETVIEYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
QY 181 SOC 183
Db 181 SOC 183

RESULT 7

US-10-243-739-39
; Sequence 39, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-243-739-39

Query Match 98.5%; Score 956; DB 15; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.5e-86;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKFGATVALLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKFGATVALLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFQLLWFHISCLTFGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFQLLWFHISCLTFGTETVIEYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
QY 181 SOC 183
Db 181 SOC 183

RESULT 8

US-10-244-065-39
; Sequence 39, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard

; APPLICANT: Pumpens, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Part
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-244-065-39

Query Match 98.5%; Score 956; DB 15; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.5e-86;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKFGATVALLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKFGATVALLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFQLLWFHISCLTFGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFQLLWFHISCLTFGTETVIEYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180
QY 181 SOC 183
Db 181 SOC 183

RESULT 9

US-09-929-955-11
; Sequence 11, Application US/09929955
; Patent No. US20020136740A1
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; APPLICANT: Catharina Hultgren
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
; FILE REFERENCE: TRIPEP.23AUS2
; CURRENT APPLICATION NUMBER: US/09/929,955
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/705,547
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/225,767
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis B virus C antigen and e antigen
; OTHER INFORMATION: (HBCag/HBeAg) sequence
US-09-929-955-11

Query Match 98.5%; Score 956; DB 10; Length 212;
Best Local Similarity 98.9%; Pred. No. 1.8e-86;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALQAIL 60
 |||||
 Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALQAIL 89
 |||||
 Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGKFRQLLWFHISCLTFTGTVIEYLV 120
 |||||
 Db 90 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGKFRQLLWFHISCLTFTGTVIEYLV 149
 |||||
 Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRPGSPRRRTSPRRRSQSPRRRSQSRE 180
 |||||
 Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSQSPRRRSQSRE 209
 |||||
 Qy 181 SQC 183
 |||||
 Db 210 SQC 212

RESULT 10

US-10-104-966-11

Sequence 11, Application US/10104966

Publication No. US20020155124A1

GENERAL INFORMATION:

APPLICANT: Matti Sallberg

APPLICANT: Catharina Hultgren

TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND

FILE REFERENCE: TRIPEP.23AUSC1

CURRENT APPLICATION NUMBER: US/10/104,966

PRIOR FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/705,547

PRIOR FILING DATE: 2000-11-03

PRIOR APPLICATION NUMBER: 60/229,175

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11

LENGTH: 212

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Hepatitis B virus C antigen and e antigen

OTHER INFORMATION: (HBCag/HBeAg) sequence

US-10-104-966-11

Query Match 98.5%; Score 956; DB 14; Length 212;
 Best Local Similarity 98.9%; Pred. No. 1.8e-86;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALQAIL 60
 |||||
 Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALQAIL 89
 |||||
 Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGKFRQLLWFHISCLTFTGTVIEYLV 120
 |||||
 Db 90 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGKFRQLLWFHISCLTFTGTVIEYLV 149
 |||||
 Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRPGSPRRRTSPRRRSQSPRRRSQSRE 180
 |||||
 Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSQSPRRRSQSRE 209
 |||||
 Qy 181 SQC 183
 |||||
 Db 210 SQC 212

RESULT 11

US-09-848-616-102

Sequence 102, Application US/09848616

Publication No. US20030054010A1

GENERAL INFORMATION:

APPLICANT: Sebbel, Peter

APPLICANT: Dunant, Nicolas

APPLICANT: Bachmann, Martin
 APPLICANT: Tissot, Alain
 APPLICANT: Lechner, Franziska
 TITLE OF INVENTION: Molecular Antigen Array
 FILE REFERENCE: 1700.0180002
 CURRENT APPLICATION NUMBER: US/09/848,616
 CURRENT FILING DATE: 2001-05-05
 NUMBER OF SEQ ID NOS: 186
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 102
 LENGTH: 183
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 OTHER INFORMATION: human Hepatitis B construct
 US-09-848-616-102

Query Match 98.2%; Score 954; DB 11; Length 183;
 Best Local Similarity 98.4%; Pred. No. 2.4e-86;
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALQAIL 60
 |||||
 Db 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALQAIL 60
 |||||
 Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGKFRQLLWFHISCLTFTGTVIEYLV 120
 |||||
 Db 61 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGKFRQLLWFHISCLTFTGTVIEYLV 120
 |||||
 Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRPGSPRRRTSPRRRSQSPRRRSQSRE 180
 |||||
 Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSQSPRRRSQSRE 180
 |||||
 Qy 181 SQC 183
 |||||
 Db 181 SQC 183

RESULT 12

US-10-243-739-42

Sequence 42, Application US/10243739

Publication No. US20030091593A1

GENERAL INFORMATION:

APPLICANT: Bachmann, Martin F.

APPLICANT: Stornl, Tazio

APPLICANT: Lechner, Franziska

TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of Immune Responses Induced by Virus Like Particles

FILE REFERENCE: 1700.0210001

CURRENT APPLICATION NUMBER: US/10/243,739

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 60/318,967

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PatentIn version 3.1

SEQ ID NO 42

LENGTH: 183

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic human Hepatitis B virus core protein gene

US-10-243-739-42

Query Match 98.2%; Score 954; DB 15; Length 183;
 Best Local Similarity 98.4%; Pred. No. 2.4e-86;
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALQAIL 60
 |||||
 Db 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALQAIL 60
 |||||
 Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYVNTNMGKFRQLLWFHISCLTFTGTVIEYLV 120
 |||||

Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
QY 181 SQC 183
Db 181 SQC 183

RESULT 13

US-10-244-065-42
; Sequence 42, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofs, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Partic
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 42
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic human Hepatitis B virus core protein gene
US-10-244-065-42

Query Match 98.2%; Score 954; DB 15; Length 183;
Best Local Similarity 98.4%; Pred. No. 2.4e-86;
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120
Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
QY 181 SQC 183
Db 181 SQC 183

RESULT 14

US-09-848-616-104
; Sequence 104, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter

; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 104
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-848-616-104

Query Match 98.1%; Score 953; DB 11; Length 183;
Best Local Similarity 98.4%; Pred. No. 3e-86;
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120
Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
QY 181 SQC 183
Db 181 SQC 183

RESULT 15

US-09-848-616-105
; Sequence 105, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 105
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-848-616-105

Query Match 98.1%; Score 953; DB 11; Length 183;
Best Local Similarity 98.4%; Pred. No. 3e-86;
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120
Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180

Db 121 SFGVWIRTPPAYRPPNAPILSTLETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
Oy 181 SQC 183
Db 181 SQC 183

Search completed: August 6, 2003, 09:55:03
Job time : 50 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2003, 09:42:19 ; Search time 29 Seconds
(without alignments)
266.996 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPKFGATVLLSFLP.....RRRSQSPRRRSQRESQC 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCRD_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	971	100.0	183	5	PCT-US96-10602-12
2	956	98.5	183	3	US-09-248-588-2
3	956	98.5	194	3	US-08-968-747-18
4	956	98.5	212	3	US-08-968-747-3
5	956	98.5	346	1	US-08-105-483-217
6	956	98.5	346	1	US-08-709-209-217
7	956	98.5	346	1	US-08-458-101-217
8	941	96.9	183	3	US-08-968-747-20
9	941	96.9	193	3	US-08-968-747-2
10	933	96.1	397	5	PCT-US96-10602-6
11	930.5	95.8	199	3	US-08-968-747-21
12	927	95.5	185	1	US-07-739-642-2
13	927	95.5	185	1	US-07-739-643-2
14	927	95.5	185	1	US-07-739-142-2
15	927	95.5	185	1	US-09-851-120-6
16	924	95.2	185	3	US-09-248-588-6
17	923	95.1	183	3	US-09-248-588-4
18	923	95.1	185	1	US-07-739-642-4
19	923	95.1	185	1	US-07-739-643-4
20	923	95.1	185	1	US-07-739-142-4
21	920	94.7	289	5	PCT-US96-10602-8
22	915	94.2	185	1	US-07-739-642-10
23	915	94.2	185	1	US-07-739-643-10
24	915	94.2	185	1	US-07-739-142-10
25	912	93.9	185	1	US-07-739-642-8
26	912	93.9	185	1	US-07-739-643-8
27	912	93.9	185	1	US-07-739-142-8

28	900	92.7	212	4	US-09-719-528A-4	Sequence 4, Appli
29	880.5	90.7	211	6	5196194-13	Patent No. 5196194
30	872	89.8	351	5	PCT-US96-10602-4	Sequence 4, Appli
31	787	81.1	159	3	US-08-445-585-3	Sequence 3, Appli
32	772	79.5	214	1	US-07-739-642-12	Sequence 12, Appli
33	772	79.5	214	1	US-07-739-643-12	Sequence 12, Appli
34	772	79.5	214	1	US-07-739-142-12	Sequence 12, Appli
35	767	79.0	214	1	US-07-739-642-6	Sequence 6, Appli
36	767	79.0	214	1	US-07-739-643-6	Sequence 6, Appli
37	767	79.0	214	1	US-07-739-142-6	Sequence 6, Appli
38	764	78.7	154	3	US-08-968-747-1	Sequence 1, Appli
39	764	78.7	155	3	US-08-968-747-17	Sequence 17, Appli
40	764	78.7	161	3	US-08-968-747-19	Sequence 19, Appli
41	672.5	69.3	188	3	US-09-248-588-7	Sequence 7, Appli
42	671	69.1	217	3	US-09-248-588-9	Sequence 9, Appli
43	616	63.4	346	5	PCT-US96-10602-2	Sequence 2, Appli
44	192	19.8	39	3	US-08-968-747-5	Sequence 5, Appli
45	173	17.8	305	3	US-09-248-588-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
PCT-US96-10602-12
; Sequence 12, Application PC/TUS9610602
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10602
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,814
; FILING DATE: 20-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/282001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10602-12

Query Match 100.0%; Score 971; DB 5; Length 183;
Best Local Similarity 100.0%; Pred. No. 6.9e-100;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVLLSFLPSDFPVSRRDLLDTASALYREALSEPHCSPHHTALRQAIL 60
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DB 1 MDIDPKFGATVLLSFLPSDFPVSRRDLLDTASALYREALSEPHCSPHHTALRQAIL 60

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QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLFTGTETVIEYL 120
|||||
Db 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLFTGTETVIEYL 120
|||||
QY 121 SFGWIRTPPAYPPNAPILSTLPTTVVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
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Db 121 SFGWIRTPPAYPPNAPILSTLPTTVVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
|||||
QY 181 SOC 183
|||
Db 181 SOC 183
|||

RESULT 2
US-09-248-588-2
; Sequence 2, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074537
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-248-588-2

Query Match 98.5%; Score 956; DB 3; Length 183;
Best Local Similarity 98.9%; Pred. No. 3.2e-98;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
|||||
Db 1 MDIDPYKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
|||||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLFTGTETVIEYL 120
|||||
Db 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLFTGTETVIEYL 120
|||||
QY 121 SFGWIRTPPAYPPNAPILSTLPTTVVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
|||||
Db 121 SFGWIRTPPAYPPNAPILSTLPTTVVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
|||||
QY 181 SOC 183
|||
Db 181 SOC 183
|||

RESULT 3
US-08-968-747-18
; Sequence 18, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-968-747-18

Query Match 98.5%; Score 956; DB 3; Length 194;
Best Local Similarity 98.9%; Pred. No. 3.4e-98;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
|||||
Db 12 MDIDPYKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 71
|||||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLFTGTETVIEYL 120
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Db 72 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLFTGTETVIEYL 131
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QY 121 SFGWIRTPPAYPPNAPILSTLPTTVVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
|||||
Db 132 SFGWIRTPPAYPPNAPILSTLPTTVVRRGSRPRRTTPSPRRRSQSPRRRSQSR 191
|||||
QY 181 SOC 183
|||
Db 192 SOC 194
|||

RESULT 4
US-08-968-747-3
; Sequence 3, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELECOMMUNICATION INFORMATION:
```


TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-968-747-3

Query Match 98.5%; Score 956; DB 3; Length 212;
Best Local Similarity 98.9%; Pred. No. 3.9e-98;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
DB 30 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYL 120
DB 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYL 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQRE 180
DB 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQRE 209
QY 181 SQC 183
DB 210 SQC 212

RESULT 5
US-08-105-483-217
Sequence 217, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Paolletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105.483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-105-483-217
Query Match 98.5%; Score 956; DB 1; Length 346;
Best Local Similarity 98.9%; Pred. No. 7.7e-98;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
DB 164 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 223
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYL 120
DB 224 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYL 283
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQRE 180
DB 284 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQRE 343
QY 181 SQC 183
DB 344 SQC 346

RESULT 6
US-08-709-209-217
Sequence 217, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
APPLICANT: Paolletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-209-217

Query Match 98.5%; Score 956; DB 1; Length 346;
Best Local Similarity 98.9%; Pred. No. 7.7e-98;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDDTASALYREALSPHCSPHHTALRQAIL 60
|||||
Db 164 MDIDPYKEGATVELLSFLPSDFPSVRDLDDTASALYREALSPHCSPHHTALRQAIL 223
|||||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIEYLV 120
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Db 224 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIEYLV 283
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QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
|||||
Db 284 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 343
|||||
QY 181 SOC 183
Db 344 SOC 346

RESULT 7
US-08-458-101-217
; Sequence 217, Application US/08458101
; Patent No. 5766599
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Perkus, Marion E.
; APPLICANT: Taylor, Jill
; APPLICANT: Tartaglia, James
; APPLICANT: No. 5766599ton, Elizabeth K.
; APPLICANT: Riviere, Michel
; APPLICANT: de Taisne, Charles
; APPLICANT: Limbach, Keith J.
; APPLICANT: Johnson, Gerard P.
; APPLICANT: Pincus, Steven E.
; APPLICANT: Cox, William I.
; APPLICANT: Audonnet, Jean-Christophe Francis
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; NUMBER OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,101
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2740
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-458-101-217
Query Match 98.5%; Score 956; DB 1; Length 346;
Best Local Similarity 98.9%; Pred. No. 7.7e-98;

Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDDTASALYREALSPHCSPHHTALRQAIL 60
|||||
Db 164 MDIDPYKEGATVELLSFLPSDFPSVRDLDDTASALYREALSPHCSPHHTALRQAIL 223
|||||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIEYLV 120
|||||
Db 224 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIEYLV 283
|||||
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
|||||
Db 284 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 343
|||||
QY 181 SOC 183
Db 344 SOC 346

RESULT 8
US-08-968-747-20
; Sequence 20, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-968-747-20

Query Match 96.9%; Score 941; DB 3; Length 183;
Best Local Similarity 97.8%; Pred. No. 1.5e-96;
Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDDTASALYREALSPHCSPHHTALRQAIL 60
|||||
Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDDTASALYREALSPHCSPHHTALRQAIL 60
|||||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIEYLV 120
|||||
Db 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIEYLV 120
|||||
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180

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Db 121 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
Qy 181 SQC 183
Db 181 SQC 183

RESULT 9
US-08-968-747-2
; Sequence 2, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10602-6

Query Match 96.9%; Score 941; DB 3; Length 193;
Best Local Similarity 97.8%; Pred. No. 1.6e-96;
Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLSPDFPSVRDLDTASALYREALSPHCHSPHHTALQAIL 60
Db 11 MDIDPYKEFGATVELLSFLSPDFPSVRDLDTASALYREALSPHCHSPHHTALQAIL 70
Qy 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLWFIHISCLTGTETVIEYLV 120
Db 71 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLWFIHISCLTGTETVIEYLV 130
Qy 121 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
Db 131 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSRE 190
Qy 181 SQC 183
Db 191 SQC 193

RESULT 10
PCT-US96-10602-6
; Sequence 6, Application PC/TUS9610602
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; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10602
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,814
; FILING DATE: 20-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/282001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10602-6

Query Match 96.1%; Score 933; DB 5; Length 397;
Best Local Similarity 98.9%; Pred. No. 3.3e-95;
Matches 177; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLSPDFPSVRDLDTASALYREALSPHCHSPHHTALQAIL 60
Db 1 MDIDPYKEFGATVELLSFLSPDFPSVRDLDTASALYREALSPHCHSPHHTALQAIL 60
Qy 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLWFIHISCLTGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLWFIHISCLTGTETVIEYLV 120
Qy 121 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSQR 179
Db 121 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSQR 179

RESULT 11
US-08-968-747-21
; Sequence 21, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,747
FILING DATE: 03-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08472/705001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-968-747-21

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RESULT 12
US-07-739-642-2
; Sequence 2, Application US/07739642
Patent No. 5173427
GENERAL INFORMATION:
APPLICANT: Mallonee,, Richard L.
; TITLE OF INVENTION: Vectors And Hosts With Increased
; TITLE OF INVENTION: Expression Of HBCAg
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07739,642
; FILING DATE: 19910801
; CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt,, Brian K.
; REGISTRATION NUMBER: 33,213

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; REFERENCE/DOCKET NUMBER: P-2272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-739-642-2

Query Match          95.5%; Score 927; DB 1; Length 185;
Best Local Similarity 95.7%; Pred. No. 5.3e-95;
Matches 177; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY      1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDDTASALYREALAESPEHCSPHHTALRQAIL 60
Db      1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDDTASALYREALAESPEHCSPHHTALRQAIL 60'

QY      61 CWGELMTLATWGVNLEDPASRLDLYSVYVNTNMGKLFQRLWLFHISCLTFCGETVLEVLV 120
Db      61 CWGELMTLATWGVNLEDPASRLDLYSVYVNTNMGKLFQRLWLFHISCLTFCGETVLEVLV 120

QY      121 SFGWLTPTPAYRPPNAPILSTLPETVTVRR--PGRSPRRRTSPRRRRSQSPRRRRSQS 178
Db      121 SFGWLTPTPAYRPPNAPILSTLPETVTVRRDGRSPRRRTSPRRRRSQSPRRRRSQS 180

QY      179 RESQC 183
Db      181 RESQC 185

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Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALQAIL 60
Qy 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKQRLWLFHISCLTFGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKQRLWLFHISCLTFGTETVIEYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRR--PCRSPPRRTPSPRRRSQSPRRRSQS 178
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 179 RESQC 183
Db 181 RESQC 185

RESULT 14

S-07-739-142-2
; Sequence 2, Application US/07739142
; Patent No. 5175272
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: DNA Sequences With Increased Expression
; TITLE OF INVENTION: of HBCag
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07739,142
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2271
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-739-142-2

Query Match 95.5%; Score 927; DB 1; Length 185;
Best Local Similarity 95.7%; Pred. No. 5.3e-95;
Matches 177; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALQAIL 60
Qy 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKQRLWLFHISCLTFGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKQRLWLFHISCLTFGTETVIEYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRR--PCRSPPRRTPSPRRRSQSPRRRSQS 178
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy 179 RESQC 183
Db 181 RESQC 185

RESULT 15

US-09-851-120-6
; Sequence 6, Application US/098511120
; Patent No. 6479282
; GENERAL INFORMATION:
; APPLICANT: LETOURNEUR, Odile
; APPLICANT: WATELET, Benedicte
; TITLE OF INVENTION: HBC EXPRESSION AND DIAGNOSTIC AND THERAPEUTIC USES
; FILE REFERENCE: 109455
; CURRENT APPLICATION NUMBER: US/09/851,120
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 185
; TYPE: PRT
; ORGANISM: HBV
US-09-851-120-6

Query Match 95.5%; Score 927; DB 4; Length 185;
Best Local Similarity 95.7%; Pred. No. 5.3e-95;
Matches 177; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALQAIL 60
Qy 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKQRLWLFHISCLTFGTETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKQRLWLFHISCLTFGTETVIEYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRR--PCRSPPRRTPSPRRRSQSPRRRSQS 178
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 179 RESQC 183
Db 181 RESQC 185

Search completed: August 6, 2003, 09:47:18
Job time : 30 secs

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